

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2004, 22:18:44 ; Search time 42 Seconds
(without alignments)
3093.871 Million cell updates/sec

Title: US-09-522-753-5

Perfect score: 13215

Sequence: 1 MSGSTQLVAQTWRATEPRYP.....WDEEPKPLLCQSYETLSDSE 3517

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/PTUS COMB.pep.*

6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7871	59.6	1495	4	US-09-337-384-1
2	7866	59.5	1495	4	US-08-522-726B-1
3	718	5.4	619	2	US-08-372-652-5
4	718	5.4	619	5	PCT-US95-16311-5
5	539.5	4.1	8991	4	US-08-714-741-32
6	477.5	3.6	3118	4	US-09-579-181-1
7	452	3.4	2972	4	US-09-579-181-2
8	429	3.2	1404	4	US-10-164-595-78
9	428	3.2	1363	4	US-07-757-022B-52
10	428	3.2	1404	4	US-07-757-022B-2
11	428	3.2	1404	4	US-07-757-022B-62
12	425.5	3.2	1320	4	US-07-757-022B-46
13	425.5	3.2	1320	4	US-07-757-022B-60
14	425.5	3.2	1361	4	US-07-757-022B-40
15	423.5	3.2	1320	4	US-10-164-595-58
16	423	3.2	1140	4	US-07-757-022B-104
17	422	3.2	2157	4	US-09-854-856-52
18	422	3.2	2217	4	US-09-854-856-20
19	422	3.2	2294	4	US-09-854-856-50
20	422	3.2	2354	4	US-09-854-856-18
21	421.5	3.2	1313	4	US-07-757-022B-142
22	421.5	3.2	1354	4	US-07-757-022B-48
23	419.5	3.2	1314	4	US-07-757-022B-50
24	416.5	3.2	1049	4	US-07-757-022B-58
25	410	3.1	1270	4	US-07-757-022B-44
26	410	3.1	2468	4	US-09-976-594-726
27	408.5	3.1	1038	4	US-07-757-022B-74
28	408.5	3.1	1311	4	US-07-757-022B-42
29	408	3.1	2185	4	US-09-854-856-36
30	408	3.1	2245	4	US-09-854-856-4
31	408	3.1	2322	4	US-09-854-856-34
32	408	3.1	2382	4	US-09-854-856-2
33	400.5	3.0	941	4	US-07-757-022B-14
34	400.5	3.0	1022	4	US-07-757-022B-84
35	400.5	3.0	1464	4	US-09-331-347C-21
36	395	3.0	1461	4	US-09-585-887-9
37	395	3.0	1461	4	US-09-289-578-9
38	388	2.9	1706	4	US-09-252-991A-31760
39	382.5	2.9	2294	4	US-09-252-991A-17231
40	380	2.9	3969	3	US-08-061-376-5
41	377.5	2.9	1064	1	US-08-642-255-62
42	372.5	2.8	1184	4	US-09-266-225D-18
43	369.5	2.8	2032	4	US-09-854-856-42
44	369.5	2.8	2092	4	US-09-854-856-10
45	369.5	2.8	2169	4	US-09-854-856-40
46	369.5	2.8	2229	4	US-09-854-856-8
47	367	2.8	1185	3	US-09-041-886-23
48	365	2.8	960	3	US-09-219-849-5
49	358	2.7	1618	1	US-07-853-913-4
50	351	2.7	1341	3	US-08-963-825-18
51	351	2.7	1341	4	US-09-500-811-18
52	351	2.7	1341	4	US-09-570-573-18
53	351	2.7	1341	4	US-09-548-608-18
54	350.5	2.7	2842	1	US-07-741-940-7
55	350.5	2.7	2842	1	US-08-289-548A-7
56	350.5	2.7	2842	1	US-08-452-654-7
57	350.5	2.7	2842	4	US-08-449-731-7
58	350.5	2.7	2843	1	US-08-452-655B-2
59	350.5	2.7	2843	1	US-08-452-655B-7
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61	350.5	2.7	2843	3	US-08-450-582-7
62	350.5	2.7	2973	2	US-08-821-355A-7
63	350.5	2.7	2973	2	US-09-003-687A-7
64	350.5	2.7	2973	3	US-09-136-605-7
65	349.5	2.6	2004	4	US-09-854-856-58
66	349.5	2.6	2064	4	US-09-854-856-26
67	349.5	2.6	2141	4	US-09-854-856-56
68	349.5	2.6	2201	4	US-09-854-856-24
69	346	2.6	3256	4	US-09-319-172-98
70	346	2.6	3256	4	US-09-976-594-22
71	343.5	2.6	2076	4	US-09-854-856-46
72	343.5	2.6	2136	4	US-09-854-856-14
73	343.5	2.6	2843	1	US-07-741-940-2
74	343.5	2.6	2843	1	US-08-289-548A-2
75	343.5	2.6	2843	1	US-08-452-654-2
76	343.5	2.6	2843	2	US-08-370-235A-2
77	343.5	2.6	2843	4	US-08-449-731-2
78	342	2.6	1939	4	US-09-854-856-48
79	342	2.6	1999	4	US-09-854-856-16
80	337	2.6	1911	4	US-09-854-856-64
81	337	2.6	1971	4	US-09-854-856-32
82	337	2.6	2048	4	US-09-854-856-62
83	337	2.6	2108	4	US-09-854-856-30
84	330.5	2.5	1418	3	US-08-963-825-20
85	330.5	2.5	1418	4	US-09-500-811-20
86	330.5	2.5	1418	4	US-09-570-573-20
87	330.5	2.5	1418	4	US-09-548-608-20
88	329	2.5	1476	4	US-09-252-991A-29427
89	328	2.5	1418	3	US-09-010-999-1
90	325.5	2.5	1312	3	US-09-041-886-19
91	325.5	2.5	1312	4	US-09-648-281-2
92	325.5	2.5	1312	4	US-09-707-919A-19
93	325.5	2.5	1312	4	US-09-083-268-3
94	325.5	2.5	1780	3	US-08-769-309A-5
95	325.5	2.5	1780	3	US-08-994-570-5
96	324.5	2.5	1274	4	US-09-095-443-2
97	324	2.5	1162	2	US-08-728-323A-2
98	324	2.5	1162	4	US-09-298-568-2
99	324	2.5	1162	4	US-09-410-399-2
100	309.5	2.3	1596	4	US-08-978-277A-4

ALIGNMENTS

RESULT 1			
US-09-337-384-1			
; Sequence 1, Application US/09337384			
; Patent No. 6551773			
; GENERAL INFORMATION:			
; APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES			
; APPLICANT: EVANS, RONALD			
; APPLICANT: CHEN, J.			
; TITLE OF INVENTION: TRANSCRIPTIONAL CO-REPRESSOR THAT INTERACTS WITH NUCLEAR HORMON			
; TITLE OF INVENTION: RECEPTORS			
; FILE REFERENCE: SALK1510-2			
; CURRENT APPLICATION NUMBER: US/09/337,384			
; CURRENT FILING DATE: 1999-06-21			
; PRIOR APPLICATION NUMBER: 08/522,726			
; PRIOR FILING DATE: 1995-09-01			
; NUMBER OF SEQ ID NOS: 3			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 1			
; LENGTH: 1495			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-337-384-1			
Query Match			
Best Local Similarity 59.6%; Score 7871; DB 4; Length 1495;			
Matches 1487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1031	DKEAFAAEAQKLPDPPCWTSGLPFPVPPREVIVKASPHAPDPSAFSAFYPGHPPLPLGLHD	1090
DB	9	DKEAFAAEAQKLPDPPCWTSGLPFPVPPREVIVKASPHAPDPSAFSAFYPGHPPLPLGLHD	58
QY	1091	TARPVLPRPTTINPPPLISSAKHPVLRQIGALISQGMVQLHVPYSEHAKAPVGVPTM	1150
DB	69	TARPVLPRPTTINPPPLISSAKHPVLRQIGALISQGMVQLHVPYSEHAKAPVGVPTM	128
QY	1151	GLPLMDPKLAPFSGVKQEQLSPRQAGPPESLGVPTAQEASVLRGTALGSPGGSITK	1210
DB	129	GLPLMDPKLAPFSGVKQEQLSPRQAGPPESLGVPTAQEASVLRGTALGSPGGSITK	188
QY	1211	GIPSTRVPSDAITYRGSITHTGPADVLKGTITRIIGEDSPSRDLDRGREDLSLPKGVHVI	1270
DB	189	GIPSTRVPSDAITYRGSITHTGPADVLKGTITRIIGEDSPSRDLDRGREDLSLPKGVHVI	248
QY	1271	EGKKGHVLSYEGGMSVTQCSKEDGRSSGPPHETAAPKRTYDMGGRVGRAISSASIEGL	1330
DB	249	EGKKGHVLSYEGGMSVTQCSKEDGRSSGPPHETAAPKRTYDMGGRVGRAISSASIEGL	308
QY	1331	MGRAPRERSPHLKEOHHRIGSITQGIPIRSVVEAQEDYLREAKLLKREGTPPPPPPS	1390
DB	309	MGRAPRERSPHLKEOHHRIGSITQGIPIRSVVEAQEDYLREAKLLKREGTPPPPPPS	368
QY	1391	RLTEAYKTQALGPLKXPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGS	1450
DB	369	RLTEAYKTQALGPLKXPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGS	428
QY	1451	ITQGTPLKVDGTASTGSKKHVDVRSILIGSPGRTFPPVHPLDVNADARALACRYESLKS	1510
DB	429	ITQGTPLKVDGTASTGSKKHVDVRSILIGSPGRTFPPVHPLDVNADARALACRYESLKS	488
QY	1511	RPGTASSSGSIARGAPVIVPELKGKRSQPLTYEDHGAPAGHLPGRGSPVTWREPTPRLO	1570
DB	489	RPGTASSSGSIARGAPVIVPELKGKRSQPLTYEDHGAPAGHLPGRGSPVTWREPTPRLO	548
QY	1571	EGSLSSSKASQDRKLASTPREIAKSPHSTVPEHHHPISPYEHLRLGVSGVDLYRSHIPL	1630
DB	549	EGSLSSSKASQDRKLASTPREIAKSPHSTVPEHHHPISPYEHLRLGVSGVDLYRSHIPL	608
QY	1631	AFDPTSIPRGIPLDAAAAYLPHRLAPNTYPHLYPPYLRGYPDPTAALENRQTIINDYI	1690

DB	609	AFDPTSIPRGIPLDAAAAYLPHRLAPNTYPHLYPPYLRGYPDPTAALENRQTIINDYI	668
QY	1691	TSQOMHNTATAMAOADMLRGLSPRESSLANYAAGPRGIIDLQOVPHLPVLVPTPTCT	1750
DB	669	TSQOMHNTATAMAOADMLRGLSPRESSLANYAAGPRGIIDLQOVPHLPVLVPTPTCT	728
QY	1751	PATAMDRLAYLPTAQPFSSSRHSSSPLSPGGGTHLTTPKTTTSSSRERDRDRDRDR	1810
DB	729	PATAMDRLAYLPTAQPFSSSRHSSSPLSPGGGTHLTTPKTTTSSSRERDRDRDRDR	788
QY	1811	EKSILTTTVEHAPIWRPGTEQSSSGSSGGGSSSRPASHAHQHSPISTRQDA	1870
DB	789	EKSILTTTVEHAPIWRPGTEQSSSGSSGGGSSSRPASHAHQHSPISTRQDA	848
QY	1871	LOORPSVLHNTGMKGIITAVEPSKPTVLRSTSTSPVRPAATFPATHCPLGTTLDGVTP	1930
DB	849	LOORPSVLHNTGMKGIITAVEPSKPTVLRSTSTSPVRPAATFPATHCPLGTTLDGVTP	908
QY	1931	TLMEPVLLPKEAPRVARPERPRADTGHAFKAPPARSGLEPASPSKSGSEPRPLVPPVSG	1990
DB	909	TLMEPVLLPKEAPRVARPERPRADTGHAFKAPPARSGLEPASPSKSGSEPRPLVPPVSG	968
QY	1991	HATARTPAKULAPHHASPDPAPPASASDPHREXTQSKPFSIOELSLSLGHSSSYSP	2050
DB	969	HATARTPAKULAPHHASPDPAPPASASDPHREXTQSKPFSIOELSLSLGHSSSYSP	1028
QY	2051	EGVEPVSPVSSPLTHDKGLPKHLELDKSHLEGLRKPQPGPKVLGGAAHLPHLRPLP	2110
DB	1029	EGVEPVSPVSSPLTHDKGLPKHLELDKSHLEGLRKPQPGPKVLGGAAHLPHLRPLP	1088
QY	2111	ESQPSSSPLLOQTAPGVKGHQRVVTLAQHISEVITQDYTRHHQPQLSAPLAPLYSPFGAS	2170
DB	1089	ESQPSSSPLLOQTAPGVKGHQRVVTLAQHISEVITQDYTRHHQPQLSAPLAPLYSPFGAS	1148
QY	2171	CPVLDIRPPSDLYLPDPDHGAPARGSPHSEGGKSPENKTSVLGGSDGIEPVSPPEG	2230
DB	1149	CPVLDIRPPSDLYLPDPDHGAPARGSPHSEGGKSPENKTSVLGGSDGIEPVSPPEG	1208
QY	2231	MTEPGHSRANVPLVRYDGEQTEPSRMGSKSPGNTSQPPAFPSKLTESNANVSKKQBI	2290
DB	1209	MTEPGHSRANVPLVRYDGEQTEPSRMGSKSPGNTSQPPAFPSKLTESNANVSKKQBI	1268
QY	2291	NKKLATHNRNEPEYINISQFTEIFNNPAITGTGLMYRSQAVOEHAHNMGLEAIRKAL	2350
DB	1269	NKKLATHNRNEPEYINISQFTEIFNNPAITGTGLMYRSQAVOEHAHNMGLEAIRKAL	1328
QY	2351	MCKYDQWEESSPLSANAFNPLNASASLPAAMPITTAADGSDHLLTSPGGGGKAKVSGRS	2410
DB	1329	MCKYDQWEESSPLSANAFNPLNASASLPAAMPITTAADGSDHLLTSPGGGGKAKVSGRS	1388
QY	2411	SRKAKSPAGLASGRPPSVSVHSEGCNRRRTPLTNRWEDRPSAGSTPPPYNPLNR	2470
DB	1389	SRKAKSPAGLASGRPPSVSVHSEGCNRRRTPLTNRWEDRPSAGSTPPPYNPLNR	1448
QY	2471	LOAGVNASPPPLPAGSGPLAGPHAMDEEPKLLCSQYETLSDSE	2517
DB	1449	LOAGVNASPPPLPAGSGPLAGPHAMDEEPKLLCSQYETLSDSE	1495

RESULT 2
US-08-522-726B-1
; Sequence 1, Application US/08522726B
; Patent No. 6489441
; GENERAL INFORMATION:
; APPLICANT: Evans, Ronald M.
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: TRANSCRIPTIONAL CO-REPRESSOR THAT
; TITLE OF INVENTION: INTERACTS WITH NUCLEAR HORMONE RECEPTORS AND USES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Precty, Schroeder, Brueggemann & Clark

STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/522,726B
FILING DATE: 01-SEP-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Reiter, Stephen E.

REGISTRATION NUMBER: 31,192

REFERENCE/DOCKET NUMBER: P41 90042

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-546-1995

TELEFAX: 619-546-9392

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1495 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: both

MOLECULE TYPE: protein

US-08-522-726B-1

Query Match 59.5%; Score 7866; DB 4; Length 1495;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1486; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1031	DKEAFAAEAQKLPDPCPTSGLPFPVPREVTKASPHAPDPSAFVAPPGHPLPLGLHD	1090
DB	9	DKEAFAAEAQKLPDPCPTSGLPFPVPREVTKASPHAPDPSAFVAPPGHPLPLGLHD	68
QY	1091	TARPVLPRPTTISNPPPLISSAKHPSVLERQIGAIISQGMVSQVLIHVPYSEHAKAPVGPVTM	1150
DB	69	TARPVLPRPTTISNPPPLISSAKHPSVLERQIGAIISQGMVSQVLIHVPYSEHAKAPVGPVTM	128
QY	1151	GLPLPMDPKKLAPFSGVKEQELSPRQAGPPESLGVPTAQEASVLRGTALGSPVGGSIYK	1210
DB	129	GLPLPMDPKKLAPFSGVKEQELSPRQAGPPESLGVPTAQEASVLRGTALGSPVGGSIYK	188
QY	1211	GIPSTRVPSDSATYRGSITHTGTPADVLYKGTITRIIGEDSPSLDRGREDSLPKGHVY	1270
DB	189	GIPSTRVPSDSATYRGSITHTGTPADVLYKGTITRIIGEDSPSLDRGREDSLPKGHVY	248
QY	1271	EGKKGHVLSYEGGMSVTQCSKEDGRSSGPPHETAAPKRTYDMMEGRVGRATISSASIEGL	1330
DB	249	EGKKGHVLSYEGGMSVTQCSKEDGRSSGPPHETAAPKRTYDMMEGRVGRATISSASIEGL	308
QY	1331	MGRAIPPERHSPHLKEQHIRGSIITQGIPIRSVVEAQEDYLRREAKLLKREGTPPPPPPS	1390
DB	309	MGRAIPPERHSPHLKEQHIRGSIITQGIPIRSVVEAQEDYLRREAKLLKREGTPPPPPPS	368
QY	1391	RDLTEAYKQALGPKLKEAHEGLVATVKEAGSIHEIPREELRHTPELPLAPRPLKEGS	1450
DB	369	RDLTEAYKQALGPKLKEAHEGLVATVKEAGSIHEIPREELRHTPELPLAPRPLKEGS	428
QY	1451	ITQGTPLKYDTGASTTSGSKKHVRSRLIGSPGRTPFPVHPDLVMDADARALACRYESLKS	1510
DB	429	ITQGTPLKYDTGASTTSGSKKHVRSRLIGSPGRTPFPVHPDLVMDADARALACRYESLKS	488
QY	1511	RPGTASSSGSIARGAPVIVPELGKPRQSPQLTYEDHGAPAGHLPGRGSPVTWREPTPRLO	1570
DB	489	RPGTASSSGSIARGAPVIVPELGKPRQSPQLTYEDHGAPAGHLPGRGSPVTWREPTPRLO	548
QY	1571	EGSLSSKASQDRKLTSTPREIAKSPHSTVPEHHPHIPSPYEHLLRGVSGVDLYRSHIPL	1630
DB	549	EGSLSSKASQDRKLTSTPREIAKSPHSTVPEHHPHIPSPYEHLLRGVSGVDLYRSHIPL	608

QY	1631	AFDPTSIPIRGIPIDAAAAAYLPRHILAPNPTYPHLYPPYLIIRGYPDPTAALENROTIINDYI	1690
DB	609	AFDPTSIPIRGIPIDAAAAAYLPRHILAPNPTYPHLYPPYLIIRGYPDPTAALENROTIINDYI	668
QY	1691	TSQOHHNTATAMAOADMRLGLSPRESSLALNYAGPRGIIDLSOVPHLPVLVPTPGT	1750
DB	669	TSQOHHNTATAMAOADMRLGLSPRESSLALNYAGPRGIIDLSOVPHLPVLVPTPGT	728
QY	1751	PATAMDRLAYLPTAQPPSSRRHSSPLSPGGPHTLTKPTTTSSSERERDRDRDRDR	1810
DB	729	PATAMDRLAYLPTAQPPSSRRHSSPLSPGGPHTLTKPTTTSSSERERDRDRDRDR	788
QY	1811	EKSILTTTVEHAPIWRPTEQSSGSSGSSGSSGSSGSSSRPASHSHAHQHSPIRPTQDA	1870
DB	789	EKSILTTTVEHAPIWRPTEQSSGSSGSSGSSGSSGSSSRPASHSHAHQHSPIRPTQDA	848
QY	1871	LOORPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPATHCPLGGLDGVVP	1930
DB	849	LOORPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPATHCPLGGLDGVVP	908
QY	1931	TLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEPASSPSKSGSEPRPLVPVSG	1990
DB	909	TLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEPASSPSKSGSEPRPLVPVSG	968
QY	1991	HATIARTPAKNLAPHHASDPDPAPPASADPHREKTQSKPFSIQELELSGLVHGSSYSP	2050
DB	969	HATIARTPAKNLAPHHASDPDPAPPASADPHREKTQSKPFSIQELELSGLVHGSSYSP	1028
QY	2051	EGVEPVSPVSSPSLTHDKGLPKHLBELDKSHLEGLRKPQPGVKLGGAHPLPHLRPLP	2110
DB	1029	EGVEPVSPVSSPSLTHDKGLPKHLBELDKSHLEGLRKPQPGVKLGGAHPLPHLRPLP	1088
QY	2111	ESQPSSSPLLOTAPGVKGHQRVVTLLAQHISEVITQDYTRHHPOQLSAPLPAPLYSPFGAS	2170
DB	1089	ESQPSSSPLLOTAPGVKGHQRVVTLLAQHISEVITQDYTRHHPOQLSAPLPAPLYSPFGAS	1148
QY	2171	CPVLDLRRPPSDLYLPPDPHGAAPRSGPSEGGKSPENKTSVLGGGEGDIEPVPSPPEG	2230
DB	1149	CPVLDLRRPPSDLYLPPDPHGAAPRSGPSEGGKSPENKTSVLGGGEGDIEPVPSPPEG	1208
QY	2231	MTEPGHRSANVPLLYRDGEQTEPSRMGSKSPGNTSOPPAFFSKLTESAMVSKKQEI	2290
DB	1209	MTEPGHRSANVPLLYRDGEQTEPSRMGSKSPGNTSOPPAFFSKLTESAMVSKKQEI	1268
QY	2291	NKKLANTHNRNEPEYINISQGTIFNMPAITGTGLMTYRQAVQEHASTWNGLAIIRKAL	2350
DB	1269	NKKLANTHNRNEPEYINISQGTIFNMPAITGTGLMTYRQAVQEHASTWNGLAIIRKAL	1328
QY	2351	MCKYDQWEESSPPLSANAFNPLNASASLPAAMPITTAADGRSDHTLTSPGGGKAKVSGRPS	2410
DB	1329	MCKYDQWEESSPPLSANAFNPLNASASLPAAMPITTAADGRSDHTLTSPGGGKAKVSGRPS	1388
QY	2411	SRKAKSPAPGLASGDRPPSVSVHSEGDGNCNRRPTPLNRRWEDRPPSAGSTPPPNLIMR	2470
DB	1389	SRKAKSPAPGLASGDRPPSVSVHSEGDGNCNRRPTPLNRRWEDRPPSAGSTPPPNLIMR	1448
QY	2471	LOAGVWASPPPLPAGSGPLAGPHHAWDEEPKPLLCSQVETLSDSE	2517
DB	1449	LOAGVWASPPPLPAGSGPLAGPHHAWDEEPKPLLCSQVETLSDSE	1495

RESULT 3

US-08-372-652-5

; Sequence 5, Application US/08372652

; Patent No. 5932699

; GENERAL INFORMATION:

; APPLICANT: Moore, David

; APPLICANT: Seol, Wongi

; APPLICANT: Choi, Hwang-Sik

; TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING

; TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS

; NUMBER OF SEQUENCES: 17

QY 2241 VYLLYRDGEQTEPRSMGSKSPNTSQPPAFFSKLTESNAMYKSKQBEINKLINTHRN 2300
Db 344 SMLLSQGVDAEQRSDSRSPGISYLPFFTKL-ESTSPMVKSKQEIFRKLNSGGG 402
QY 2301 EPEYNISQCTEIPFNPAITGTGLMTYRQAOEHAHTNMGLEAIRKALMGYQDWE- 2359
Db 403 DSDMAAQPGTEIFNPAVTSIGAVSRSHSFADPAS-NUGLEDIIRKALMGFDDKVED 461
QY 2360 -----SPPLSANAFNPLNASASLPAAMPITAAQGRSDHTLTSPPGGG-GKAKVSRPSSRK 2413
Db 462 HGVVMSHPV---GIMPGSASTSV-----VTSSEARRDBGEPSPHAGVCCKPLINKNSRK 513
QY 2414 AKSPAPGLA--SGDRPSSVSVSHSEGCNRRTPLTNRWEDRPSAGSTPPFNPLMLRL 2471
Db 514 SKSPIQGSYLGTERPSSVSHSEGDYHRTQTP--GWAWEDRPSSTGCTOFFYNPLTIRM 571
QY 2472 QAGWASPPPGPLPAGSGPL--AGPH---HAWDEPKPLCSOYETLSDSE 2517
Db 572 ----LSSTPTQIACAPSAITQAAPHQONRIWEREPAPLLSAQYETLSDSD 618

RESULT 5

US-08-714-741-32
; Sequence 32, Application US/08/714741
; Patent No. 6500613
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
; TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,741
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2460
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8991 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-714-741-32

Query Match 4.1%; Score 539.5; DB 4; Length 8991;
Best Local Similarity 18.5%; Pred. No. 1.4e-21;
Matches 551; Conservative 312; Mismatches 1122; Indels 1001; Gaps 116;

QY 116 PLLRPSPLLATGQAGSGLTDKRSITGKLEPVSPSPHTDPELELVPPLRSK-BELIQ 174
Db 5314 PAPAPKPELKEIDESDSEVVKE---GFRAPL-----QSEDAKQAKLSKEELSD 5361
QY 175 NMDRVREITWVQOI-----SKLKKQOOLEE 202
Db 5362 KIDELDAEIAKLEDDQKAAEENNVVDYFKEGLEKTIAAKKAELKTEADLKAANVEPK 5421
QY 203 EAAKPEPEKPVSPPIESKHSRLVQIIVDENRKKAAAHRILEGGLGPOVELPYNQPSD 262
Db 5422 PKEPSQPEKPAEAPPEQP-----TEPTQPEKPAEQOPAPAPQEKPAEETPAP 5473
QY 263 TRQYHENIKINQAMRKILYFKRRNHARKQWKFCQ-----YDQLEALEKVKVRIEN 318
Db 5474 KPE-----KPAEQPKAEKPAEQABEDYARRSEBYNRLTQPPKAEKAPAP 5520
QY 319 NPARRAKESKVRHY-----YEKQF--PEI-----RKORELQRMQRVSG 355
Db 5521 APKTGGSALDQEAAPPHQVADLEKQITGPEIFLGADPEADIAARPNELAAK-QAELA 5579
QY 356 QRGSGI-----SMSAARSSEHYSEIIDGL-SEQENLEKQMRQLAVIPML 399
Db 5580 QKPTGLEKLLSDLPCKGTQDELKKEAGAEALDKADELPNKVADLEKESINLEI---LL 5636
QY 400 YDADQORIKFINNGLMADPMKYKDRVMNMWSEQEKETFRKFMQHPKNFGLIASFLE 459
Db 5637 GGADSE-----DDTAALPNKL-----AKKXAELEKTKELDAAPNELGPDGD--E 5679
QY 460 RKTVAECVLYITKKNENYKSLVRRSRRRGKSKQO-----QOQOQOQOQOQOQMPRS 535
Db 5680 EETPAP-----APQEQOPAPAPKPEQOPAPAPKPEQOPAPAPKPEQOPAPAP 5732
QY 516 SOBEKDEKEKEAEKEEKPEV-----ENDKEDLLKXKTD 553
Db 5733 KPEQAPKPEKPAEPTQPEKPATPKTRVRAKVAEFGVQLRDAGGNNVGAYPEGUEET 5792
QY 554 SGE-----DNDEKEAV----- 564
Db 5793 TAEXEAGLKGAADLKKAVIDEPETPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 5952
QY 565 -----ASKGRKTANSQGRKGRITRSMANBANSEBAITPOQSAELASHELNE 611
Db 5853 PAPAPKAPAPAPAPAPKPEKPA-----PAPKPEPTKTKLIDESD 5895
QY 612 SSRWTEE-----EMETAKKGLLEHGRNWSAIAIRMGVSKTVSQCKNFYFNKQKQNL 663
Db 5896 SEDYAKEGRLAPLQSELDTKKAKLLK-----LEELSG-----KIEELD 5933
QY 664 EILQCHKLMEKERNARRKKKAPAAASBEAAPPVVEDEMEASGVSGNEEMVEBEA 723
Db 5934 AEIXELEVL-----KDAEGNNVVEAYFKEGLEKTTAB-----KKALEKAE 5976
QY 724 LHASGNEVPRGCSGPATVNSSDTESIPSPHTEAAKOTGONGPKPATLADGPPPGP- 782
Db 5977 DLKKAVIDEPETPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 6022
QY 783 --PTPPRTSRAPIEPTASEATGAPTPAPAP-PSPSAPPVVPVPEKEEETAAAPVEE 839
Db 6023 PKPAPAPKAPAPAP-KPAPAPKAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 6081
QY 840 ---GEOQKPPAAAEELAVDTGKAE-----PVKSEC-----TEEAPEGPAKGD 881
Db 6082 TPKTGWKQENGMLKE--IDESDSEYVKGFRAPLQSELDKQAKLSKEEXSDKXDEL 6139
QY 882 AAEATAEALKAEKKEGG--SGRATTAKSGAPQSDSSATSCADVDVBAEGGDKNRLLS 939
Db 6140 AEIAKLEKDVDFKNSDGEQAGYLA-----AEEDLIKAKKAEALKEKKA 6191
QY 940 PRPSLLTPTGDRANASQKPLDLKQKORAAIP-PIQVTKVHEPPREDAAPTAPPA 998
Db 6192 PETPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 6250

QY 999 PPPPQNLQ-----ESDAP-----QPGSSPRGSRSPAPPADKFAFAEAQKL 1042
 Db 6251 APAPKEKPAALKEIDESEVVKAELELVKEAEKEPRNEEKVKQAKAEVESKKAETRL 6310
 QY 1043 P-----GPPCWTSGLPVPVPPREVIKASPHAPDPSAPSYA-- 1078
 Db 6311 EKI KTRKKAEBAKRAAEEDKVKKEPA-----PKPENPAEQPKAEKADQQAEDYARR 6365
 QY 1079 -----PPGHPLPLGLHDTARVPLPRP-----TISNPPPLISSAK 1113
 Db 6366 SBEEXELTQQQPP-----KTEKPAQSTPKTKGEARESRXEEKVNQPKXEVESKK 6416
 QY 1114 HPSVLERQICAIQSQMSVOLHPYISHAKAPVGTWGLPLPM-DPKKLAPESGVKQSQL 1172
 Db 6417 XEATRLKTI-KTRDKKAEAXRAAEEDKVKKEPAEQPOQAPAPQPEKPA----- 6466
 QY 1173 SPRGQAGPESLGVPTAQEASVLRTGALSGVPGSITKGIPSTRVPSDAITYRGSITGH 1232
 Db 6467 -----APKPEN-----PAEQ-----PKAEKPADQ-----QAEEDYA 6492
 QY 1233 TPADVLYKGTITRIIGEDSPSLDRGREDSLPKGHVYIEGKKGHVLSY-EGMSVTVQCSK 1291
 Db 6493 RRSEEEYNR-----LTQQQPPKTEKPAQSTTK-----IKEXDESXSBDYLKEGLRAPLQSK 6544
 QY 1292 EDGRSSGPPHETAAPKRTYDMMEGRVGR-AISSASIEGLMGRAIPPERHSPHLLKEQHH 1350
 Db 6545 LDTKKAKLSKLELSDK--IDELDAEIAKLEVLQDAEG-----NNN 6584
 QY 1351 IRGSITOGIPRSVVEAQEDYLRREAKLLKREGTPPPPPSRDLTEAYKTOALGPLKLKPA 1410
 Db 6585 VEAYFKEGLEKTTAEKAELEKAEADLKKAVDEPETAPA-----PQAPAPAEKPA 6635
 QY 1411 HEGLVATVKBAGRSIHIPREELRHPTPLAPRP-----LKEGSITQ 1453
 Db 6636 EKAPAPAEKPAPEKPAPEKPA-----TPEKD-APTPTPTKGWQENGMMYFYNNDGSMAT 6690
 QY 1454 GTPLK-----YDTGASTTG-----SKKHD-----VRSLLG 1478
 Db 6691 GWLQNGSYYLNSNGAMATGWQHNQNSWYLYNSLKEIDESESDYLKEGLRAPLQSKLD 6750
 QY 1479 SPGRTPFPVHPLDMADARALACRYEESLKSRRP-----TASSGGSIAIR 1524
 Db 6751 TKKAKLSKLELSDKIDELDAEIAKLEVLQDAEGNNVEAYFKEGLEKTTAEKAELEK 6810
 QY 1525 G-----APVIVPELGKQSPSLTYEDHGAPFAGHLPRGSPVTMRPTPR 1568
 Db 6811 AEADLKXAVDEPDTAPAQAPAPAEKPAPEKPA-----AP-APEKPAPE-----EKPA 6861
 QY 1569 LOEGSLSSSK-ASQDKLTSTPREIAKSPHSTVPEHHPHIPISPYEHL----- 1614
 Db 6862 PEKPAPEKPAPEKPAPEKPAPEKPAPEKPA-----PKPETPTRLTRKRYLKEIDES 6919
 QY 1615 -----LRGVSGVOL 1623
 Db 6920 DSEYDLKEGLRAPLQSKLDTKKAKLSKLELSDKIDELDAEIAKLEVLQDAEGNNVEA 6979
 QY 1624 Y-----RSHIPLAFDPTSIPRGIPLDAAAAY----- 1650
 Db 6980 YFKEGLEKTTAEKAELEKAEADLKKAVDEPETAPAQAPAPAEKPAPEKPAPEKPA 7039
 QY 1651 -----LPRHLAFNPTVPHLYP-----PYLRGY 1673
 Db 7040 APEKPAPEKPAPEKPAPEKPAPEKPAPEKPAPEKPAPEKPAPEKPAPEKPAPEKPA 7099
 QY 1674 ---PDTAALENQTIINDYITSQMHNTATAMACQADMLRGLSPR-----BSSL 1720
 Db 7100 RAPLQSKLDKAKKLSKLELSDKIDELDAEIAKLEVLQDAEGNNVEAYFKEGLEKTI 7159
 QY 1721 ALNYAAGPRGIIDLQVPHLPVLVPTPTGTATAMDRILAYLFT-APQFSSRHSSPLSP 1779
 Db 7160 AAKKAELEKTEADLKKAVNEPEKPAPEKPAPEKPAPEKPAPEKPAPEKPAPEKPA 7213
 QY 1780 GGPHTLTKPTTSSSERDRDRDREREKKSILTS-----TTTVEHAPIWRPGTEQSSG 1836

Db 7214 EKPAEQPKETKDDQQAEDYARRSEEEYNR-----LTQQQPPKAEKPAAPAPKTGWKQENG 7269
 QY 1837 -----SSGSSGGGGSSSPASHAHQHSPISPRTQDALQORPSVLHNTGKGIITAV 1890
 Db 7270 MWYFNTDGMGEQAGYRAAAEGDLAAKQAELEKTEAD-----LKKAVN-- 7314
 QY 1891 EPSKPTVLRTSTSSPVVRPAATPPATHCPLGGTLGCVYPTLMEPVLLPKPEAPRVARP-E 1949
 Db 7315 EPEKPA--PAPETPAPAPAEQPKPA-----PAPQAPAPAEKPEKPAE 7354
 QY 1950 RPRADTGHAFIA-----KP-PARSGLEPASSP--SKGSEPR 1982
 Db 7355 QPKAEKTDQQAEDYARRSEEEYNRLTQQQPPKAEKPAPEKPEQAPAPAKNSKGQAE 7414
 QY 1983 PLVPVPSGH-----ATTARTPAKNLAPHASPPDAPPAS 2017
 Db 7415 QYRSAAGGDLAAKQVELEKTEADLKKAVNEPEKPAPEKPAPEKPAPEKPAPEKPA 7474
 QY 2018 ASDPHREKTQ---SKPFISIQ---ELELSLGYHGSSYSPEGVEPVSPVSPSLTHDKGLP 2071
 Db 7475 APKEKPAEQKAEKPADQQAEDYDRRSBEEYNRLTQQQPPKAEKPAPEKPEQAPAP 7534
 QY 2072 KHLBELDKSHLEGEIRP--KOPGPVKLGGEAAHLPHLRPL-----PESOPSSPLIQTAPG 2125
 Db 7535 KSLKEIDESDESDEYVYKEGFRAPLQSELDKQAKLSKLELSDKIDELDAEIAKLEKQVED 7594
 QY 2126 VK---GHORVVTLAQHISEVI-----TDYTRHHHPQQLSAPLAPLYSPFGASCFLV 2174
 Db 7595 FKXSDGEGAGQGYLAAAEEDLAKKAELEQTEADLKKAVNEPEKPAPEKPAPEKPA 7653
 QY 2175 DLRRPSPDLYLPPPDHGPARGSPHSEGGKRSPPBNTKSVLGGGEDGIEPVSPGEMTEP 2234
 Db 7654 --EQPK-----PAPETPAPA--PKPEKPAEQPKPEK-----PADQQAEE 7689
 QY 2235 GHRSAAVPLLYRDEGEQTEPSRMGSKSPGNTSOP-----PAFFSKLTSNSAMVSKS 2286
 Db 7689 DYARES-----BEEYNRLTQQQPPAKQBPQAPKPEKPAEETQPEKDAEIAKLE 7738
 QY 2287 KQ-EINKLNTNHRNEPEYNTISQPGTEIFNPAITGTGLMTYRQAOVQEHASTNGL--- 2342
 Db 7739 KNVEYFKKTDABQTSQ-----YLAIAEKDLADKKAELEK 7773
 QY 2343 EAIIRKALMGKYDQWNEESPPLSANAFNPLNASASLPAAMPITAADGRDHTLITSPGGGK 2402
 Db 7774 EADLKKAVNEPEKPAEETP-----APAPKP----- 7798
 QY 2403 AKVSGRPSRKAAPAGLSDGDRPPSVSVHSEGDGDCNRRTPLT-NRYWEDRPSA---G 2458
 Db 7799 ----EQAPQKPAPEKPAPEKPAPEKPAPEKPAPEKPAPEKPAPEKPAPEKPA 2504
 QY 2459 STFPFYNPLIMLQAGVWASPPPPGLPAGSGPLAGPHHAWDEEKP 2504
 Db 7855 PAPKBPQVPAEXPENPAPAPAPAXAPQ---PLKPEEPA--EOPKP 7895

RESULT 6
 US-09-579-181-1
 ; Sequence 1, Application US/09579181
 ; Patent No. 6365372
 ; GENERAL INFORMATION:
 ; APPLICANT: Chivia, John
 ; APPLICANT: Yaciuk, Peter
 ; TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
 ; FILE REFERENCE: 16153-4247
 ; CURRENT APPLICATION NUMBER: US/09/579,181
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/136,620
 ; PRIOR FILING DATE: 1999-05-27
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 3118

; TYPE: PRT		
; ORGANISM: Human		
US-09-579-181-1		
Query Match		3.6%; Score 477.5; DB 4; Length 3118;
Best Local Similarity		18.6%; Pred. No. 1.3e-18;
Matches 597; Conservative 330; Mismatches 1109; Indels 1169; Gaps 136;		
QY	137	KORSLTGKLEPVSPPH--TDP-----EELVPPRLSKBEL-IQNMDRVDRDI 183
DB	2	QDSLDG-----PPGPDGATVLEGFSLSQADLANKGPKWEKSHAEIAEQAKHEAEI 55
QY	184	TMVEQIISKKKKQOQLEBAAPPEKP-----VSPPTIESKH-----R 224
DB	56	---ETRIAEIRKEGFWSLKRLKVPPEPPREPKGHWDYLCEEMQWLSADFAQERWRKRGVAR 112
QY	225	SLVQI1---YDENRKAEEAAHRTLEGLGPOVELPLYNQPSDTRYHENIKINQAMRKKLI 281
DB	113	KVVRWIRHHEORQKEERAREQA---KLRIASTMAKDVQFWSNV-----EKV 161
QY	282	LYFKRNHARKOWKQFCORYDQIMEALEKKVERIENNRRAKESKV-----329
DB	162	VQFKQSRLEKKKALDLHLDFIVQTEKYSDLLSQSLNQPLTSSKAGSSPCIGSSAA 221
QY	330	-----REYKEQPEIRKQRE-----L 346
DB	222	SSPPPPASRLDDGDGFQPOEDEEEDDEETIEVEEQEGNDABEAQRREIELLRREGELPL 281
QY	347	QERMSRVGQSGS-LSMSAARSEHEVSEIIDGLSEQENLEKQMQO-LAVIPWLYDAQ 404
DB	282	ELLRLSPOLLEGGSPSPOTSSHD-SDTRDG-PEEGAEPPQVLEIKPPP--SAVT 336
QY	405	ORLKFNNMGLMADPMKVYKDRQVNMNWSQOEKTEFREKFMQHPKMFGLIASFLERKTV 464
DB	337	QRNK-----QPHPDDEDEFTA-NEEBAEDBEDTIAEEQLEGEVDHAMELSELA 386
QY	465	-----ECVLYYL-----TKQNYKSLVRRSYRRRGSKSQOQOQOQOQOQOQ 509
DB	387	REGELSMELLQYAGAYAPGSGSEDEDEVDANSSDCEPEGPVEABEPPOEDSSQS 446
QY	510	QMPRSQOEKEKEKEA-----EKEEKPEVENDKEDLLKEKTDTSQ-----E 556
DB	447	DSVEDSEDEEBSHEEETSGSASESESESEDAQSOSQADEBEEDDFGVYLLAR 506
QY	557	DNDEKAVASKGRKT-----ANSQRRKG-----590
DB	507	DEEQSEADAGSPPTGPTTLGPKKEITDIAAAESLQPKGYTLATVQVKTPIPLLRGQ 566
QY	581	-----RITRSMANEANSEAI-TPQQAELA-----S 606
DB	567	LREYQHIGLDWLVMTVEKKLNGILADEMGLKTIQTISLHLACEKGNWGHPLIIVPTS 626
QY	607	MELN---ESSRW-----TEEMETAKG-----LLEH-----G 631
DB	627	VMLNWEMLKRWCPFKILTYGAQERKLKQGWTKPNAFHVCITSYKLVLDQHOAFRR 686
QY	632	RNWSATARMVGSKTVOCKNF-----YFNKKR-----QV-----L 662
DB	687	KNW-----RYLILDEAQNIKFKSQRWQSLNFNFSQRRLLLTGTPLQNSLMELSMHFLM 742
QY	663	DEILQOH-----KLWMEKERNARRKK 683
DB	743	PHVFGSHREFKEWFSNPLTGMIEGSQBYNEGLVKRLHKLVRPELLRRVKVDVEKQPKKY 802
QY	684	K---KAPAAASEEAPPPVVEDEMEASGVSGNEEEMVEAEALHASGNEVPREGCSGA 740
DB	803	EHVIRCLSKRQCLYDDFMAQTTTKETLATGHFMSVINTLMQJ-----RKVCNHP- 853
QY	741	TVNNSDTESIPSP-----HTEAAKDTGONGPKPATLGADG---777
DB	854	---NLFDPRPVTSFPTPGICFSTASLVLRATDVHPLQRIIDMGFRD-----LIGLSGRVS 905
QY	778	-----PPPGP-----PTP-----PR 787
DB	906	RYEADTFLPRHLRRLVLEVATAPDPPRPKPVKMKVARMLOPVKQEGRTVVVVNNPR 965
QY	788	R-TSRAPIETPASEATGAPTPPAP-----PSPAPPPVPVPEKEEETAAP 836
DB	966	APLGPVPVPPPGPPELSAQPTGCPVQVLPASLMVSASP-AGPPLIP-ASRPPGCVLLPP 1023
QY	837	VEEGEQKPPA-ABELAVDTGKABEPVKSECTEEAEEGPAKGDAAAATASGALKAEK 895
DB	1024	LQPNSSGLPQVLPSPGLVLSGTSRPPTLSLKPTP--PAPVRLSPAPPPGSSSLKPLT 1081
QY	896	KEGSGRATTAKSSGAPQDSATCSADEVDEAEGDKNRLSPRLSLTPTGD-----950
DB	1082	VPEG-----YTFPPAAATTTTATTATTAVPAPTAPORLILSPDMQARLPSEGVVSI 1137
QY	951	-----PRANASPOKPLDLK-----QLKQ-----RAAIAIPPIQVTK-----980
DB	1138	QLASLAQRPVANAGSKPLTFQIQNKLTITGQVRLQVLAGQRPLOMPTMWNNTGVVK 1197
QY	981	--VHEPPREDAAPTKPAPPAPPQNLQPESDAQO--QPGSSPR--GKSRSPAP--1028
DB	1198	IVVRQAPRDGLTPVPLAPAPRPPSSGLPAVLNPRPTLTGRLPTTLGTARAPMPTPL 1257
QY	1029	-----PADKEAFAAEAKLPGDPPCWTSGLPFPVP-----PREVIKASPHA 1069
DB	1258	VRPLLKLVHSPSPFEVSASA-----PGAAPL-TISSPLHVPSSLPGPASSMPIPNSSPLA 1311
QY	1070	POPSAFSYAPPGHPLPLGLHDTARVLPRLPPTISNPPPLISSAKHPSVLIERQIGAISQM 1129
DB	1312	SPVSSTVSVPLSSSLPISVPTTLPAASAPLTIPIASPLTVSASGALL-----1360
QY	1130	SVQLHVPEYSEHAKAPVPTMTGLPMDPKLAPFGSVKQEOQLSPRQOAGPPES---LGV 1186
DB	1361	-----TSVTPPLAPVVPRAAPG-----PSLQPSG-ASPSASALTGL 1396
QY	1187	PTAQ---EASVLRTALGVPGGSIYKGIPISTRVPSDAITYRGSITHG-----1332
DB	1397	ATAPSLSSQTPGHPLLLAPTSHVPLGNSTVAPACSPVLVPASALASPFPSPAPNAPAQ 1456
QY	1233	---TPADVLYKGTITRIIGEDSPSLDRGREDSPKGVHY---EGKKGHVLSVEGM 1284
DB	1457	ASLLAPASASQALATPLAPMAQPTAILAPSPAPPLAPLPLVLPASGAPVLASSQTPV 1516
QY	1285	SVTQCKEDGRS--SSGP---PHETAAPKRTYDMMEGRVGRAT-SSASIEGL-MGRAIPP 1337
DB	1517	PVMAPSSTFGTSLASASVPAPTPVLAPSSQTMLPAPVPSPLPSPASTQTALALAPAL 1576
QY	1338	ERHSPHLKEQHIRGSIQGIPIRSVVEAQEDYLRREAKLLKREGTPPPPPPSRDLTEAY 1397
DB	1577	T-----LGGS-----SPSQTLSLGTGNPQGPFPPTQLS---1604
QY	1398	KTOALGPLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAP-PUKEGSIQGT 1456
DB	1605	-----LTPA-SSLVPT---PAOTLSLAPGPPGPTQLSLAPPLAPLASPVGPAP 1651
QY	1457	LKYDTGASTTGSKK---HDVRSLIGSPGRTPFPVHPLOVMDADALERACYEESLKSRP 1512
DB	1652	AHTLTILAPASSASLILAPASVQTLTUSPA-----PVPTLGPAAQTLALAPASTQSPA 1704
QY	1513	GTASSSGGIARGAPVIV-----PELGKPRQSPPLYTHEDHGAAGPAGHLPRGSPV 1560
DB	1705	SOASSILVWSASGAAPLFTVMVSRPLPVSKDEPDTLTLSRSGPPSPSTATSFSGPGRPRQP- 1763
QY	1561	TWREPTPR-----LQE-----GSLSSSKASQDRKLTSTPREIA 1593
DB	1764	---PPPRPFYLDLSLEKKRKQRSERLERIIFOLSEAHGALAPVYGVTEVLDFTCLPQVPA 1820
QY	1594	K--SPHSTVPEH-----HPHPISPYEHLRGVSGVDLYRSHIPLAFDPTSPRGI 1641
DB	1821	SPIGPRSPPGSHPTFWTYTEAAHRAVLFPQORLDQLSIEIEREIFVMP-----PVEA 1872
QY	1642	PLDAAAAYLPHRLAP-----NPTVPHLYPPYLI-----RGYPD-----1675

Db 640 LLRRVKVDKQMPKKYEHVIRCLSKRQRCLYDDFMAQTTTKETLAT-----GHF 690
QY 579 KGRIT-----RSMANEAN-----SBEAITPOQSAELASMEINNESSRWTEEMETAKG 626
Db 691 MSVINILMLQRLKVCNHNFLFDRPVTSPTTIGICFSTASLVLRAVDVHPLQIDMGFRD 750
QY 627 LLE-HGRNWSAIARMVGSKTVSOCKNPFYNYKRONLDEILOQHLKMEKERNARKKK 685
Db 751 LIGLEGR-----VGRYEADTFLPRHL-----SRRVLE 779
QY 686 APAAASEEAAFPVVEDEEMEAASGVSGNEEBEAEALHASGNEVPRGECSPATVNN 745
Db 780 VATAPD-----PRPKPVKMN-----RMQ-----PVKQGRVTVVNNP 818
QY 746 -----SDTESIPSPHTE-AAKDTQNGKFP-----PATLGADGPPPGPP-----TPPRTSRA 792
Db 819 RAPLGPVPRPPGPPELSAQPT--PGVPQVLPASLMVSASAPAGPLIPASRPPGPVLLP 876
QY 793 PIEPTPASEATGATP-----PPAP-----PSPSAPPVVPVKEEKEETAAAPVE 838
Db 877 PLOPNSGSLPQVLPFSLGVLSGTSRPTTSLKPTPPAPVRLSP-----APPPG 926
QY 839 EGEEQKPPAAEELAVDTGKAEFPVKSECTEEAEBGPAKGDAAEAATAGALKAEKKG 898
Db 927 SSSLKP-----LTVPPGYTFPP----- 944
QY 899 GSGRATTAKSSGAPQSDSATSADVEDEAGDKNRLSPRSLLITPTGD----- 950
Db 945 --AAATTT-----STTTATATTAVPAPTAPQRLIILSPDMQARLPSEGVISQOLA 994
QY 951 -----PRANASOKPLDLK-----OLKQ-----RAAAIPIQVTK-----V 981
Db 995 SLAQRPVANAGGSKPLTFQIGNKLTGQAVRQLAVGQPRQLQMPMTWNNNTGVKIV 1054
QY 982 HEPREDAAPTKAPAPPQPNQLOESDAQO---OPGSSPR---GKSRSPAP----- 1028
Db 1055 RQAPRDGLTPVPLAPAPRPPSSGLPAVLNPRPTLTGRLPTTLGTARAPMTPTLVRP 1114
QY 1029 -----PADKEAFABEAQKLPDPPCWTSGLPFPV-----PREVIKASHAPDP 1072
Db 1115 LKXLVHSPSEVSASA-----PGAAPL-TISSPLHVPSSLPGPASSPMPIPNSSPLASPV 1168
QY 1073 SAFSYAPPGLHPLGLHDTARVLPRLPPTISNPPPLISSAKHPSVLERQIGAISQGMVQ 1132
Db 1169 SSTVSVPLSSSLPISVPTLPAAPASPLTIPISAPLTVSASGPAAL----- 1214
QY 1133 LHVYPSEHAKAPGVPTMGLPLPMDPKLAPFGSVKQEQLSPRQACPPES---LGVPTA 1189
Db 1215 -----TSVTPPLAPVPAAPGP-----PSLOPSG-ASPSASALTGLATA 1253
QY 1190 Q--EASVLRGTALGSPVGGSIKGIPTSRVPSDSAITRGSITHG----- 1232
Db 1254 PLSLSSQTPGHPHLLAPTSHVPLGINSVTAPACSPVLVPASALASPPSPAPNAPQAOL 1313
QY 1233 -TPADVLYKGTITRIIGEDSPSLDRGREDSPKGVHVIY-----EGKKGHVLSEYEGMSVT 1287
Db 1314 LAPASSAQALATPLAPMAAPQTAILAPSPAPLAPLVPAPLAPSGAAPVLASSQTPVPM 1373
QY 1288 QCSKEDGRS--SSGP---PHETAAPKTYDMMEGRVCAIT--SSASIEGL-MGRAIPERH 1340
Db 1374 APSSTPTSLASAPVPAFTVPLAPSGTQTMPLPAPVPSLPSPASTQTLALAPALAPT-- 1431
QY 1341 SPHLKEQHIRGSIITQIGIPRSVVEAQEDYLRREAKLLKREGTPPPPPSRDRDTEAYKTQ 1400
Db 1432 -----LGGS-----SPSQTLSLGTGNPQGFPTQILS----- 1458
QY 1401 ALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPR-PLKEGSIITQGTPLKY 1459
Db 1459 -----LTPA-SSLVPT---PAQTLAPGPPLGPTQTLAPLAPLAPASPVGPAPHT 1508
QY 1460 DTGASTTGSKK---HDSVRLSGSPGRTFPFVPLDVMADARALERACYEESLSKSPGTA 1515
Db 1509 LTLAPASSASLLAPASVQTLTUSPA-----PVPTLGPAAQTLALAPASTQSPASQA 1561

QY 1516 SSSGGGIARGAPVIV-----PELGKPRQSPLIYVEDHGAPFAGHLPRGSPVTMR 1563
Db 1562 SSLVWSASGAAPLPTVMTWSRLPVSKDEPDTLTLRSGPPSPSTATSGGPRPRQP----- 1617
QY 1564 EPTPR-----LOE-----GSLSSKASQDRKLTSTPREIAK-- 1594
Db 1618 PPPRSPFFYLDLSELEKRGQRSERLERIFOLSEAHGALAPVYGVTEVLDFCTLQPPVASPI 1677
QY 1595 SPHSTVPEH-----HPHPISEVHLLRGVGDLYRSHIPLAFDPTSPRGIPLD 1644
Db 1678 GPRSPGSPHTFTWYTEAAHRAVLFPQRLDQOLSEIERIFVMP-----PVEAPPP 1729
QY 1645 AAAAYLPHLAP-----NPTYPHLYPYLI-----RGYPD-----TA 1677
Db 1730 SLHACHPPWLAQAAFOELASLWPRARPLHRIVCNMRTQFPDLRLIYQDCGKQLTL 1789
QY 1678 ALENRO-----TIINDYITSO-----QMHNTATAMAQADMRLG----- 1712
Db 1790 AVLLRQLKAGHRVLFTQWTRMLDVLEQFLTTHGHLYLRLDGSTRVQOALMERFNAD 1849
QY 1713 -----LSPRESSLALNVAAGPRGIIDLISOVPHLPVLVPTPTGTATAMDR----- 1757
Db 1850 KRIFCFLSTRSGGVNLTGADTVVYDSW-----NPTMDAQADRCHRIGQTR 1900
QY 1758 -----LAYLPTA-----POPFSSRHS 1773
Db 1901 DVHIYRLISERTVEENILKANKRMLGDMAIBGNFTTAYFKQOTIRELFDMPLEBPSS 1960
QY 1774 SS-PLSP-----CGPHTLTKPTTSSSERDR----- 1800
Db 1961 SSVSAPBEEETVASKQTHILEQALCRAEDEDIRAAQOAKAEVLAELAFNENDGPPA 2020
QY 1801 -----DREDRDREREKSILTSTTVEH----- 1823
Db 2021 GEGEEAGRPGAEEDEMSRAEQETAALVEQLTPRIYAMKLEASLEVSBEELKQAEQV 2080
QY 1824 -----APIWR-PGTEQSSGSG--SSGGGSSSRPASHAHQH--SPISPR 1867
Db 2081 EAARKDLQAKERVFLPQEEEGPGAGDESSCGTGGTHRRKKAKAPERPGTRVSERL 2140
QY 1868 ODALQORPSVLNTHGMKGIITAVEPSKPTVLRSTST---SSVPRPATFPFATHCPLGCT 1924
Db 2141 RGARAEQOGANHTP-----VISAHQ-----TRSTTTPRCSPARERVPRPAPRPTTAS 2190
QY 1925 LDGVYPTLMEPVLPLKEAPRVARPERPRADTGHAFLAKPPARSGLEPSSPSGSEBRPL 1984
Db 2191 APAAIAPAL---VPVPSAPVPIAPNPITILPVHILPSPPPSQIPPCSSPA--CTPPPA 2245
QY 1985 VPPVSGHATTIARTPAKNLAPHASP---DPPAPPASAS-----DPHREKTSQKPSI 2033
Db 2246 CTPPPAHTP---PPAQTCLVTPSSPLLGLGPPSVPIASVTNLPLGLRPEAELCAQALASP 2302
QY 2034 QEULESLGLVHGS-----YSPEGVFVS---PV-----SSPSLTHDKG-LPKHLE 2075
Db 2303 ESLELASVASSETSSLSLVPKDLLPVAEILFVSEKNLSLTSPASPLTLEAGSIPNGOE 2362
QY 2076 ELDKSHLEBLRPKQGPVKLGCEAAHLP-----HLRPLPESQSSPLLQTAGVKGH 2129
Db 2363 QEAPDPAEGTTLVLP-----EGEELPLCVSENGLELPPSAASDEPLOEPLADR-- 2413
QY 2130 QRVVTLAHISEVITDTRHHHPQOL-SAPLPAPLYSFPGASCFLDLRRRPPSDLYLPPP 2188
Db 2414 -----TSEELTEAKTPTSSPEKQELVTAEVAAPSTSSSATSSP----- 2452
QY 2189 DHGAPARGSPHSGGKRSPENKTSVLGGEDGIEPVSPPEGTEPGHRSASVPLLYRD 2248
Db 2453 -----EGFSPARPPR-----RRR 2465
QY 2249 GEOTEPSRMGSKSPGNTSOPPA--PFSKLTESAMVKSQKQINKLNTHNRNEPEYNI 2306
Db 2466 SADVEIRGQGTGRPG---QPPGPKVLKPLPGRLVTVVEEKELVORRR----- 2509

QY	2307	SQGTETFNPAITCGLMTYRSQAVQEHASNTMGLAIIRKALMGKYDQWEESSPLS--	2364
DB	2510	QORGAASLTIVGVSET-----SASGPSV--RSMGP-----ESSPIGPG	2549
QY	2365	-----ANAFNPLNASALPAAMP--ITAADGRSDHTLT	2395
DB	2550	CEAAPSSSLPTPOQFFIARRHIELGVTGGSPENGDGALLAITPAPKRRRRGRPPKKOR	2609
QY	2396	SPGGGKAKVGRSPSRKAKS-----PAPG-----LASGRPPSVSVSHSEG	2437
DB	2610	SPADACRGVDEAPSSSTLKGKTNAGADVPVGPETLIVADPVLRLQIPGPQPLGQPVH---	2666
QY	2438	DCNRRTPLNRYWE---DRPSSAGSTPFVNPVNLINELQAGVNAS-----PPPGGLP	2485
DB	2667	---RPNPLPSVPEKRRRRGRPPKARDLIP-----GTISSAGDGNSESRTPQPPHP	2713
QY	2486	AGSGPLAGPHHAWDEBPKPLLC	2507
DB	2714	SPLTPL-----PPLTLC	2725
RESULT 8			
US-10-164-595-78			
; Sequence 78, Application US/10164595			
; Patent No. 6657054			
; GENERAL INFORMATION:			
; APPLICANT: Origene Technologies, Inc			
; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides			
; FILE REFERENCE: IU 103 R1			
; CURRENT APPLICATION NUMBER: US/10/164,595			
; CURRENT FILING DATE: 2002-06-10			
; NUMBER OF SEQ ID NOS: 80			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 78			
; LENGTH: 1404			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-164-595-78			
Query Match 3.2%; Score 429; DB 4; Length 1404;			
Best Local Similarity 20.8%; Pred. No. 2.8e-16;			
Matches 266; Conservative 136; Mismatches 516; Indels 360; Gaps 54;			
QY	476	NYNKSLVRSYRRGKSO-----QQQQQQQQQQQQQQQMPRSSQEEKDEKE	524
DB	126	SQTKSTTKKSPKPPNKKTKKVIIESEITEHSVSENQSSSSSSSSSIIRKIKSS	195
QY	525	KEKEAEKE-BEKPEVENDKEDLLKEK-----TDDT-SGEDNDEKEAVASKGRKANSQ	575
DB	186	KNSAANRELQKLVKDKNKNRTKKPTPKPPVVDEAGSLDNGDFKVTTPDTSTTQHNK	245
QY	576	GRKGRITRSMANPANEBAITP-QQSAELASMLNESSRWTEEMETAKKGLLEGRNW	634
DB	246	VSTSPKIT--TAKPINRPLPNSDTSKSTLVNKETTVETTKTTNKQTSSTDGKEK	303
QY	635	SAIARMVGSKTVSQCKNFYFNFKRQNLDELQOHLKME---KERNARRKKKKAPAAAS	691
DB	304	TTSAKETQSTKTSKDL-----APTSKVLAKPTPKAETTTKGPAITTPKEPTTPPK	356
QY	692	EEAAPPPVVEDEMEASGVSGNEEBMVEEABALHASGNEVPRGECSPATVNNSSDTESI	751
DB	357	EPASTTP-----KEPT-----PTTIKSAPTTTPE	380
QY	752	PSPTTEAAKOTGONGKPPATLGADGPPPGPTTTPRTSRAPIBPTPASEATGAPTPP--	809
DB	381	PAPTTTTSAPTTTPEKAPTTT-----KEPAPTTTPEKAPTTTKEPATT-TKSAPTTTPE	434
QY	810	PAPPSAPPVVPVPEKEKEEETAAAPPVVEEGEQKPPAAEELAVDTGKAEPEVKSECTEE	869
DB	435	PAPTTTPEKAPTTTPE--PAPTTTPEKAPTTTPEKAPTTTPEKAPTTTPEKAPTTTPE	485
QY	870	AEBGPAKGDAAEABTAEGALKAEKKGSGRATTAKSSCAPQDSSSATCSADEVDEA	929

DB	486	APKPAPTTPEKAPTTTPEKAPTTTKE-----PSPTTPEKAPTTTTSAPTTTKEP	537
QY	930	EGGDKNRLSRRPSLLTPTGDPANASPOKDLDLKQLKQRAAAIPPIQVTKVHEP----	985
DB	538	-----APTTTKSAPTTTKEP-----SPTTTKEPAPTTT	565
QY	986	REDA--APTKPAPAPPPQNLQPEDAPQOFGSSPRGSKSRSPAPPADKEFAFAEAQKLP	1043
DB	566	KEPAPTTTPEKAPTTTPEKAPTTTPEKAPTTTPEKAPTTTPEKAPTTTPEKAPTTT	625
QY	1044	GDPP-----CWTSGLPFPVPPREVIKASPHADPSAFSAPCHPLPLGLHDTARVLP	1099
DB	626	PTTPEKAPTTTPEKAPTTTPEELAPTTTPEPTT-----PEEPAPT-TPKAAADNTPE	679
QY	1100	PTISNP-PPLISSAKHPSVLERIQIGAIQSGMSVQLHVPVSEHAKAP-----VGPVTMGLP	1153
DB	680	PAPTTTPEKAPTTTPEKAP-----PTTPEKAPTTTPEKAPTTTPEKAPTTTPEK	720
QY	1154	LPMDPKLAPFSGVKQEQOLSPRGQAGPPESL---GVPTAQEASVLRGTALGVSPOGSI	1210
DB	721	APTTPKKDAP-----KELAPTTTKEPTSTTCDKPAPTT-----KGTA-----	758
QY	1211	GIPSTRVPSDSAITYRGSITHTGTPADVLYKGTITRIIGEDSPSLDRGDESLPKGHVIY	1270
DB	759	--PTT--PKBPAPT-----TPKEPAPTTTPEKAPTTTPEKAPTTTPEKAPTTT	804
QY	1271	EGKKGHVLSYEGGMSVTCQSKEDGRSSGPPHETA--APKRTYDMMEGRVGRASIASIE	1328
DB	805	-----TTTKGPTSTT-----SDKPAPTTPEKAPTTTPEKAPTTTPEKAPTTT	850
QY	1329	GLMGRAP--ERHSPHILKEQHHRGSIITOGIPRSVVEAQEDVLRREAKLLKEGTP-	1384
DB	851	-----PPTTSEVSTPTTTTKEPTTIHKSPDESTPE-----LSAEPPTK	887
QY	1385	-----PPPPSRDLTEAYKTQALGPLKLPKPAHGLVATVKEAGRSIHEIPREELRHTPE	1439
DB	888	ALENGKPEGVPTTKT-----PAATKE-----MTTAKD-----KITERDLRTTPT	931
QY	1440	PLAPRLKEGSIT-----QGTPLKYDGTGAS-----TTGSKK	1470
DB	932	TAAPKMTKETATTTTEKTSKITATTTQVTSITTTQDTPFKITTLTKTLAPKVVTTTKT	991
QY	1471	HVRSLLIGSPGTFPPVPHLDVMDARALERACYESLSKSRPCTASSSGS-IARGAPVI	1529
DB	992	ITTTTETMKNPEET-----AKXDRATNSKATTPKPKPKPKPKPKPKPKPKPKPK	1039
QY	1530	VPBLGKPROSLTYEDHGAPFAGHLPGRGSPVTMRE--PTPRLQEGSLSS--KASQDRK	1584
DB	1040	MPVRKAPKTP-----TPRKMSTMPELNFTSRIAEAMLQTTTTRPNQTPNSK	1086
QY	1585	LT-----STPREIAKSPHSTVPBHHPH-----PISPYEHLRGVSGVDLYRS	1626
DB	1087	LVEVNPKESEDAGAEGETPHMLLR-PHFVMPVEVTPMDYLPVFNQGIIN-----	1136
QY	1627	HPLAPDPTSPGIFLD	1644
DB	1137	--PMLSDETNCNGKXPD	1152
RESULT 9			
US-07-757-022B-52			
; Sequence 52, Application US/07757022B			
; Patent No. 6433142			
; GENERAL INFORMATION:			
; APPLICANT: Gesner, Thomas G.			
; APPLICANT: Clark, Stephen C.			
; APPLICANT: Turner, Katherine			
; APPLICANT: Hewick, Rodney M.			
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors			
; NUMBER OF SEQUENCES: 143			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Genetics Institute, Inc.			
; STREET: 87 CambridgePark Drive			

CITY: Cambridge		
STATE: Massachusetts		
COUNTRY: U.S.A.		
ZIP: 02140		
COMPUTER READABLE FORM:		
MEDIUM TYPE: Floppy disk		
COMPUTER: IBM PC compatible		
OPERATING SYSTEM: PC-DOS/MS-DOS		
SOFTWARE: Patent In Release #1.0, Version #1.25		
CURRENT APPLICATION DATA:		
APPLICATION NUMBER: US 07/757,022B		
FILING DATE: 19910910		
CLASSIFICATION: 530		
PRIORITY APPLICATION DATA:		
APPLICATION NUMBER: US 07/643,502		
FILING DATE: 18-JAN-1991		
PRIORITY APPLICATION DATA:		
APPLICATION NUMBER: US 07/546,114		
FILING DATE: 29-JUN-1990		
PRIORITY APPLICATION DATA:		
APPLICATION NUMBER: US 07/457,196		
FILING DATE: 29-DEC-1989		
PRIORITY APPLICATION DATA:		
APPLICATION NUMBER: US 07/390,901		
FILING DATE: 08-AUG-1989		
ATTORNEY/AGENT INFORMATION:		
NAME: Cseri, Luann		
REGISTRATION NUMBER: 31,822		
REFERENCE/DOCKET NUMBER: GI 5190		
TELECOMMUNICATION INFORMATION:		
TELEPHONE: (617)876-1170		
TELEFAX: (617)876-5851		
INFORMATION FOR SEQ ID NO: 52:		
SEQUENCE CHARACTERISTICS:		
LENGTH: 1363 amino acids		
TYPE: AMINO ACID		
TOPOLOGY: linear		
MOLECULE TYPE: protein		
US-07-757-022B-52		
Query Match		3.2%; Score 428; DB 4; Length 1363;
Best Local Similarity		20.8%; Pred. No. 3.1e-16;
Matches		266; Conservative 136; Mismatches 516; Indels 360; Gaps 54;
QY	476	NYKSLVRSYRRRGKSO-----QQQQQQQQQQQQQQQMPRSSOEEKDEKE 524
DB	85	SQTIKSTTKSPKPPNKKTKKVIIESEITEHSVSENQSSSSSSSSSTIWKKS 144
QY	525	KEKEAEKE-EEKEVENDEKDLKSK-----TDDT-SGEDNDEKEAVASKRKTANSQ 575
DB	145	KNSAANRELQKLVKNDKNKRTKKKPTKPPVVVDGAGSLDNGDFKVTTPDTSTTQHNK 204
QY	576	GRKKGHITSMEANSEEAITP-QQSALASMEINNESSRWTEEMETAKKGLLEHGRNW 634
DB	205	VTSPPKIT--TAKPINRPSLSPNSDTSKTSITVKNKTTTETTKTTNNKQTSFDGKEK 262
QY	635	SAIARVMGKTVSOCKNFYFNKKRQNLDEILOQHLKME---KERNARRKKKKAPAAAS 691
DB	263	TTSAKETQSIKTSADL-----APTSKVLAKPTPKAETTTKGALTPPKPTTTPK 315
QY	692	EEAAPPVVEDEMEASGVSGNEEMVVEBAALHASGNVPRGECGSPATVNNSSDTSI 751
DB	316	EPASTTP-----KEPT-----PTTIKSAPTTPKE 339
QY	752	PSPHTEAAKDTGONGPKPATLGADGPPGPPPTPRRTSRAPLEPTPASEATCAPTP-- 809
DB	340	PAPTTTKSAPTTPKEAPTTT-----KEPAPTTTPKEPAPTTTTPKEPAPTT-TKSAPTTPKE 393
QY	810	PAPPSPSAPPVVPKKEKEEATAAAPVEEGEBQKPPAAAEELAVDTGKAEPEPKSECTEE 869
DB	394	PAPTTPKKAPPTPKB--PAPTTPKBPTTTPKEPAPTTTPKEPAPTTTPKEPAPTT----- 444
QY	870	ABEGPAKGDAAEAATAEGALKAEKKGSGRATTAKSGAGPQDSGAPQDSGATCSADEVDEA 929

DB	445	APKKPAPTTTPKEPAPTTTPKEPAPTTTKE-----PSPTTPKEPAPTTTTSAPTTPKEP----- 496
QY	930	EGGDKNRLSPSLLTPTGDPANASPOKFLQKQKRAAAIPIPIQVTKVHEP-----P 985
DB	497	-----APTTTKSAPTTPKEP-----SPTTTPKEPAPTTTP 524
QY	986	REDA--APTKPAPPAPPQNLQOPESDAPQOQSGSPRGSKSRSPAPPADKBAFAAEAKQJP 1043
DB	525	KEPAPTTPKKAPPTTPKEPAPTTTPKEPAPTTTKKPAKPAPKEPAPTTTPKETAPTTPKLT 584
QY	1044	GDPP-----CWTSGLPFPVPPREVIKASPHAPDPSAFSYPAPPHPLGLGLDHTARVULPRP 1099
DB	585	PTTPEKLAPTTPEKAPPTTPEELAPTTPEEPTTT-----PEEPAPT-TPKAAAPNTPKE 638
QY	1100	PTISNP-PPLISSAKHPSVLERQIGAISQGMVSQVLHPVHYSEHAKAP-----VGPVTMGLP 1153
DB	639	PAPTTTPKEPAPTTTPKEPAP-----PTTPKETAPTTTPKGATPTTLKEP 679
QY	1154	LPMDPKKLAPFSGVKOEQLSPRQAGPPBSLG---VPTAQEASVLRGATLGSVPGGSITK 1210
DB	680	APTTPKKAP-----KELAPTTTKEPTSTSDKAPPTTP-----KGTA----- 717
QY	1211	GIPSTRVPSDSAITYRGSTHGTTPADVLYKGTITRIIGEDSPRLDRGREDSLPKGHVY 1270
DB	718	--PTT--PKAPAPT-----TPKEPAPTTTPKGATPTTLKEPAPTTTPKKPAPKELAP----- 763
QY	1271	EGKKGHVLSVEGGMSTQCSKEDGRSSSGPPPHETA--APKRTYDMMEGRVGRVSAISSASIE 1328
DB	764	-----TTTKGPTSTT-----SDKAPPTTPKETAPTTTPKEPAPTTTPKKPAPTTPETP-- 809
QY	1329	GLMGRAIPP---ERHSPHHLKEQHHRGSIITQIPRSYVEAQEDYLRRREAKLKRCTP- 1384
DB	810	-----PPTTSEVSTPTTTPKEPTTIHKSPDESTPE-----LSAETPK 846
QY	1385	-----PPPPSRDLTEAYKTOALGPLKPKAHEGLVATVEAGRSIHIEPREELRHPTPE-L 1439
DB	847	ALENSPKFPGVPTTKT-----PAATKPE---MTTTAKD-----KTERDLRTTPTT 890
QY	1440	PLAPRLPKESGIT-----QGTPLKYDTGAS-----TTGSKK 1470
DB	891	TAAPKMTKATATTTKTESKITATTTQVSTTTQDTTTPFKITTLKTTLAPKVTTKT 950
QY	1471	HDVRSLIGSPGRTFPVPHPLDVMDARALERACYBSLSKSRPGTSSSGGS-IARGAPVI 1529
DB	951	ITTEIMNKPEET-----AKPDRAINSKATTPKPKQPKTKAPKPTSTKKPKT 998
QY	1530	VPGLKPROSPLTYEDHGAPFAGHLPRGSPVTWRE--PTPRLOEGSLSSS---KASQDRK 1584
DB	999	MPRVKPKTTP-----TPRKMTSTMPELNPTSRIAEAMLOTTTRENQTPNSK 1045
QY	1585	LT-----STPREIAKSPHSTVPEHHPH-----PISPYEHLHGVSGVDLYRS 1626
DB	1046	LVEVNPKSDAGAEGETPHMLLR-PHFVMEVPTPDMOYLPRVFNQIILN----- 1095
QY	1627	HIPLAFDPTSIPIRGIPLD 1644
DB	1096	--PMLSDETINCKGKVD 1111

RESULT 10
US-07-757-022B-2
; Sequence 2, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.

Mon Apr 19 08:15:00 2004

STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cseri, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-2

Query Match 3.2%; Score 428; DB 4; Length 1404;
Best Local Similarity 20.8%; Pred. No. 3.2e-16;
Matches 266; Conservative 136; Mismatches 516; Indels 360; Gaps 54;
QY 476 NENKSLVRRYRRGKSO-----QQQQQQQQQQQQQQQPMRSSQEEKDEKE 524
DB 126 SQTIKSTTKRSPKPNKKTKKVBEEITEHVSSENQSSSSSSSSSSSSSTIWKIKSS 185
QY 525 KEKEAEKE-EKPEVENDKEDLLKEK-----TDDT-SGEDNDEKAVASKGRKTANSQ 575
DB 186 KNSAANRELQKLKVKONKKNKTKKTPKPPVVDVDEAGSLDNGDFKVTTPDTSTTQHNK 245
QY 576 GRRKGRITRSMANSEASEATP-QQSAELASMLNNESSRWTEEMETAKGLLEHGRNW 634
DB 246 VSTSEKIT-TAKPINRPSLPNPSNDTSKETSATVNETTETVETKETTNNKQTSDDGKEK 303
QY 635 SAIAIMVCKSVQCKNPFYNYKKQNLDLILQOHLKME---KERNARRKKKAPAAAS 691
DB 304 TTSAKETOSIEKTSADKL-----APTSKVLAKPTKPAETTKGPAITTKPTTPPK 356
QY 692 EEAAPPVVVEEMEASGVSGNEEMVEAEALHASGNVPRGBCSGPATVNNSSDTESI 751
DB 357 EPASITP-----KEPT-----PTTIKSAPTPKE 380
QY 752 PSPTEAAKDTQCGKPKPATLGADGPPGPTTPRRTSRAPIEPTPASEATGAPTP-- 809
DB 381 PAPITTKSAPITPKPAPITP-----KBPATTPKEPAPITPKPAPITP-TKSAPITPK 434
QY 810 PAPPSRAPPVVVPEKEEKEETAAAPPVEEGEQKPPAAELAVDGTGAEPVKSCTEE 869
DB 435 PAPITPKKAPITPKP-----PAPITPKPTTPKEPAPITPKPAPITPKPAPITP----- 485

QY 870 AEEGPAGKDAEAAEATAEGALKAEKKEGSGSRAITAKSSGAPQDSDSATCSADEVDEA 929
DB 486 APKKPAPITPKPAPITPKPAPITPKPAPITPKPAPITPKPAPITPKPAPITPKPAPITPKP 537
QY 930 EGGDKNLLSPRPSLLTPTGDPANASPOKPLDLKQLKQRAAAIPIPIQVTKHEP--P 985
DB 538 -----APITTKSAPITPKP-----SPTTKEPAPITP 565
QY 986 REDA--APTTPAPPAPPPQNLQEPADPOQPGSSPRGKSRSPAPPADKFAFAEAKLP 1043
DB 566 KEPAPITPKPAPITPKPAPITPKPAPITPKPAPITPKPAPITPKPAPITPKPAPITPKP 625
QY 1044 GPPP-----CWTSGLPFPVPPREVIKASPHADPSAFSAPGHPPLPLGLHDTARPVLRP 1099
DB 626 PTTPEKLAPITPKPAPITPEELAPITPEBPTPT-----PEEPAPITPKPAPITPKP 679
QY 1100 PTISNP-PPLISSAKHPSVLEROIGALSQMSVQLHVHPYSEHAKAP-----VGVTMTGLP 1153
DB 680 PAPITPKPAPITPKPAPITPKPAPITPKPAPITPKPAPITPKPAPITPKPAPITPKP 720
QY 1154 LPMDPKKLAPFSGVKQOLSPRGQAGPPESLG---VPTAQEASVLRGTALGSPVGGSIK 1210
DB 721 APTTPKKPAP-----KELAPITTKPTSTSDKPAITP-----KGTA----- 758
QY 1211 GIPSTRVPSDAITVRGSIHTGTPADVLYKGTITRIGEDSPSLDRGSDSLPKGHVY 1270
DB 759 --PTT--PKPAPIT-----TPKEPAPITPKPAPITPKPAPITPKPAPITPKPAPITPKP 804
QY 1271 BGKKGHVLSYEGGMSVTQCKEDGRSSSGPPHETA--APKRTYDMMGRVGRGAISSASIE 1328
DB 805 -----TTTKGPTSTT-----SDKPAITPKPAPITPKPAPITPKPAPITPKPAPITPKP 850
QY 1329 GLMGRAIPP---ERHSPHLKEQHHRGSIITQGIIPRSRVEAQEDYLREAKLLKEGTP- 1384
DB 851 -----PPTTSEVSTPTTKEPTTIHKSPPDESTPE-----LSAEPKPK 887
QY 1385 -----PPPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPRELRHTPE-L 1439
DB 888 ALENSPKBEGVPTTKT-----PAATKPE---MTTAKD-----KITERDLRTTPTT 931
QY 1440 PLAPRPLKEGSIT-----OGTPLKYDTGAS-----TTGSKK 1470
DB 932 TAAPKMTKETATTEKTTESKITATTTQVSTTTQDTTPTFKITTLTKTLTLPKVTITTKT 991
QY 1471 HDVRSLSGPGTTPFPVHPDLVMDARALERACYESLSRPGTASSGGS-IARGAPVI 1529
DB 992 ITTTEIMNKPEET-----AKPKDRATNSKATTPKPKPKPKPKPKPKPKPKPKPKPKPK 1039
QY 1530 VPBLGPROSLTYEDHGAPFAGHLPGRSPVVTMRE--PTPRLOEGSLSSS---KASQDRK 1584
DB 1040 MPVRKPKTTP-----TPRKMTSTMPELNPTSRIAEAMLOTTTRPNOTPNSK 1086
QY 1585 LT-----STPREIAKSPHSTVPEHHH-----PISPYEHLRLGVSGVDLYRS 1626
DB 1087 LVEVNPKESEDAGAEGETPHMLLR-PHVFMPEVTPDMOYLPRVPOGIIIN----- 1136
QY 1627 HIPLAPDPTSIPIGLD 1644
DB 1137 --PMLSDETNICNGKPDV 1152

RESULT 11
US-07-757-022B-62
; Sequence 62, Application US/07/757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cseri, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-46

Query Match	3.2%;	Score	425.5;	DB	4;	Length	1320;
Best Local Similarity	21.2%;	Pred. No.	4.1e-16;				
Matches	261;	Conservative	127;	Mismatches	491;	Indels	355;
						Gaps	53;
QY	508	QQQPMPSQEQEKEKEKEAEKEEKPEVNDKEDLLKEK-----TDDT-SGEDND	559				
DB	93	KRSKP-----PNKKTKTKVIESEBITVKNKNRKTKKPTKPPVVDAGSLGD	145				
QY	560	EKEAVASGRKMTANSQGRKRIFRSMANSEAEATP-QQSAELASMELNESSRWTEE	618				
DB	146	DPKVTPDTSTTHKNVSTSPKIT--TAKPINRPSLPNSDTSKETSITVNKETTVEK	203				
QY	619	EMETAKGILLEGHRNWSAIAARMVGSKTVSQCKFYFNFKRONLDBILOQHKLME---	675				
DB	204	EYTTINKQTSIDGKEKTSISAKETQSIKTSAKDL-----APTSKVLAKPTKAEYTTK	256				
QY	676	ERNARRKKKAPAAASEBAAPPPVVEDEEMASCVSGNEEMVEEAEALHAGSNEVP	735				
DB	257	GPALTTPKEPTPTTKPEPASTTP-----KEPT--	283				
QY	736	CSGPATVNNSSDTEISPSPHTEAAKOTQNGPKPPATLGADGPPPGPTPPRRTSRAPTE	795				
DB	284	---PTTIKSAPITPKPEAPTTTKSAPITPKPEAPTTT-----KEPAPITPKPEAPITTK	335				
QY	796	PTPASEATCAPTPP--PAPPGSPAPPPVVPVKEEKEEETAAAPVBEGBEQKPPAAEELAV	853				
DB	336	PAPTT--TKSAPITPKPEAPITPKKDPAPITPK--PAPITPKPTPTTPKPEAPITTK	392				
QY	854	DTCKABEPVKSECTEABEGPAKGDPAFAEATAGALKAEKKEGGSGRATTAKSSGAPQ	913				

RESULT 13
US-07-757-022B-60
; Sequence 60, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive

Mon Apr 19 08:15:00 2004

ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19910910
APPLICATION NUMBER: US/07/757,022B
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cseri, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G1 5190
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1361 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-40

Query Match 3.2%; Score 425.5; DB 4; Length 1361;
Best Local Similarity 21.2%; Pred. No. 4.3e-16;
Matches 261; Conservative 127; Mismatches 491; Indels 355; Gaps 53;
QY 508 QQQWPRSSQEEKEKEAEKEEKEPEVNDKEDLLKEK-----TDDT-SGEDND 559
DB 134 KRSPK-----PNKKTKKVIIESEITEVKONKNTKKKPPKPPVVDGAGSLDNG 186
QY 560 EKEAVASKGRKTANSQGRKRITRSMANESSEAITP-QQAAELASMLNNESSRWTEE 618
DB 187 DFKVTPDTSITQHNKYSTSPKIT--TAKPINRPSLPNSDTSKETSLSLVNKETTVEIK 244
QY 619 EMETAKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNKKRQNLDELLOQHLKME---K 675
DB 245 ETTTNTQSTGDKETTSKETSIEKTSKADL-----APTSKVLAKETPKAETTK 297
QY 676 ERNARRKKKAPAAASEEAPPPVVDDEMEASGVSGNEEMVEEAEALHASGNEVPRGE 735
DB 298 GPALTTPKEPTTPKEPASITP-----KEPT-- 324
QY 736 CSGPATVNNSSDTEISPSHTEAAKDTQCGKPPATLGADPPGPTTPRRTSRAPIE 795
DB 325 ---PTTIKSAPTTPKEPATTTKSAPTTPKEPATTT-----KBPATTPKEPATTTKE 376
QY 796 PTPASEATCAPTPP--PAPPSAPPPVVPVVEEKEEETAAAPPVEEGEQQPPAAEELAV 853
DB 377 PAPT--TKSAPTTPKEPATTPPKKAPATPKP--PAPTTPKEPTTPKEPATTPKBPAP 433
QY 854 DTGKAEPVKSECTEAEAGPAKGDAAAEATAGALKAEKGGSGRATKSSGAPQ 913
DB 434 TTPKEPAT-----APKKPATTPKBPATTPKEPATTTKE-----PSPTTPKEPAT 482
QY 914 DSDSATCSADEVDEAGDKNRLSPRSLTTPGDPANASPOKPLDLKQLKQRAAAI 973
DB 483 TTKSAPTTKBP-----APITTKSAPTTPKEP----- 509

QY 974 PPIQVTKVHEP-----PRED--APTKPAPPAPPPQNLQFESDAPQQPQSSPRGSRSPA 1027
DB 510 ---SPTTTKEPATTPKEPATTPKBPATTPKBPATTPKBPATTPKBPATTPKBPATTPKBP 566
QY 1028 PPADKEAFAAEAQKLPDPP-----CWTSGLPPFPVPPREVIVKASPHAPDPSAFSAPRGHP 1083
DB 567 PTPKETAAPTTPKKLPTTPPEKLAPTTPKBPATTPPEELAPTTPPEBPTTP-----PEEP 621
QY 1084 LPGLHDTARVLPRPPTISNP--PPLISSAKHPSVLERQICAI SQGMSVOLHVPVSEHAK 1142
DB 622 APT--TPKAAAPNTKBPATTPKBPATTPKBPATTPKBPATTPKBPATTPKBPATTPKBP 661
QY 1143 AP-----VGPVTMGLPLPMDPKKLAPSGVQKQOLSPRQAGPPESLG---VPTAQEASV 1194
DB 662 APTTPKGTAPTTPKBPATTPKBPATTPKBPATTPKBPATTPKBPATTPKBPATTPKBPATTP 711
QY 1195 LRGTALGSPVGGSTIKGIPSTRVPSDSAITYRGSITHGTADVLKYGTITRIIGEDSPSR 1254
DB 712 -KGTA-----PTT--PKBPAT-----TPKEPATTPKGTAPTTPKBPATTP 750
QY 1255 LDRGREDSLPKGHVIEGKKGHVLSEYGGMSVTCQSKEDGRSSSGPPHETA--APKTYD 1312
DB 751 PKKPAPKELAP-----TTTGGPTSTT-----SDKPATTPKETAAPTTPKBPAP 793
QY 1313 MMEGRVGRATISSASIEGLMGRAIPP---ERHSPHLKEQHIIHRSITQGI PRSYVEAQED 1369
DB 794 TTPKKPAPTTPETP-----PPTTSEVSTPTTTPKEPTTIHKSPDESTPE----- 836
QY 1370 YLRKAKLLKEGTP-----PPPPSRDLTEAYKTQALGPLKLPKAPHAEGLVATVKEAGRS 1424
DB 837 -----LSAEPKPALENSKPEGVPTTKT-----PAATKPE---MTTAKD--- 874
QY 1425 THEIPREELRHTPE-LPLAPRLPKESIT-----QGTPLKXDT 1461
DB 875 --KITTERDLRTTPTTTAAAPKMTKETATTTTEKTESKITATTTQVTTSTTQDTPPKITT 932
QY 1462 GAS-----TTGSKKHVRSILGSPGRTFPFVPHLPDVMADARALACYSLSKSRPGT 1514
DB 933 LKTTTTLAPKVTTKTKTITTTTEIMNKPEET-----AKPDRAINSKATTPKPKQ 980
QY 1515 ASSSGGS-IARGAPVIVPELKGPROSPLTYEDHGAPFAGHLPRGSPVTMRE--PTPRLOE 1571
DB 981 PTKAPKPTSTTKKTPMVRVKPTTP-----TPKMTSTMPELNPTSRIAE 1027
QY 1572 GSLSS--KASQDRKLT-----STPREAKSPHSVTVPEHHH-----PISP 1610
DB 1028 AMLQTTTRNPQTPNSKLVENPKSEDAAGGETPHMLLR-PHVFMPEVTPMDVLPV 1086
QY 1611 YEHLRGVSGVDLYRSHPILAFDPTSI PRGIPLD 1644
DB 1087 NQGIIN-----PMLSDETINCGKPPVD 1109

RESULT 15
US-10-164-595-58
; Sequence 58, Application US/10164595
; Patent No. 6657054
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; FILE REFERENCE: IU 103 R1
; CURRENT APPLICATION NUMBER: US/10/164,595
; CURRENT FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 58
; LENGTH: 1320
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-164-595-58
Query Match 3.2%; Score 423.5; DB 4; Length 1320;
Best Local Similarity 21.2%; Pred. No. 5.4e-16;

126 SQTIKSTTKRSPKPNKKTKKVIIESEITEHSVSENQESSSSSSSSSSSSSTIWKIKS 185
525 KEKEAEKE-EEKPEVENDKEDLLKEK-----TDDT-SGEDNDEKEAVASKGRKTANSQ 575
186 KNSAANRELQKLLKVKDNKNKTKKPTPKPPVVDGAGSLDNGFKVTTPTDTSITQINK 245
576 GRKGRITRSMANEANSEBAITP-QOSAEIASMEINLESRWTEEMETAKGLLEHGRNW 634
246 VTSPPKIT--TAKPINRPSLPSNDSKETSILTWNKETTIVETKTTTTNNKQTSDDGKEK 303
635 SAIAWMVGKTSVQCNKFNKVRQNLDEILLOQHKLME-----KERNARRKKKAPAAAS 691
304 TTSKETSQSTKETSADL-----APTSKVLAKPTPKAETTTKGPALTTPKEPTTPPK 356
692 EEAAPFVVEDEMEASGVSGNEEVEAEALHASGNEVPRGECGSPATVNNSSDTSI 751
357 EPASTTP-----:-----KEPT-----PTTIKSAPTTPKE 380
752 PSPTTEAAKDTGONGPKPATLGADGPPGPPPTPRRTGRAPIEHTPASEATGATPP-- 809
381 PAPTTPKAPATTPKEPATTT-----KEPATTPKKEPATTTTKEPATTT-TPKSAPTTPKE 434
810 PAPSPSAPPVVPVKEKEBEETAAPVBEGRQKPPAAEELAVDTGKAEEVPKSECTEE 869
435 PAPTTPKAPATTPKE--PAPTTPKPTTPKKEPATTPKKEPATTPKKEPATTT----- 485
870 AEGPAGKGAEEAAEATAEGALKAKEKGGSGRATTAKSGAPQDSDSATCSADEVDEA 929
486 APKKEPATTPKKEPATTPKKEPATTTKE-----PSPTTPKKEPATTTTKEPATTTTKEP- 537
930 EGGDKNLLSPRPSLLTPTGDPNANASQKPLDLKQLKQRAAAIPIQVTKVHEP----P 985
538 -----APTTPKSAPTTPKEP-----SPTTPKKEPATTP 565
986 REDA--APTKEPATTPPPQNLOPESDAPQPGSSPRGSKRSPPADKEAFAAEAQKLP 1043
566 KEPATTPKAPATTPKKEPATTPKKEPATTTKAPKAPKAPKAPKAPKAPKAPKAPK 625
1044 GDPP-----CWTSGLPFPVPPREVIKASHPADPSAFYAPGHPPLGLHDTARVLP 1099
626 PTTPEKAPATTPKAPATTPBELAPTTPEEPPTT-----PEEPAPT-TPKAAAPNTPK 679
1100 PTISNP-PPLSSAKHPSVLERQIGALISQGMVQLHVPVYSEHAKAP-----VGPVTMGLP 1153
680 PAPTTPKAPATTPKKEP-----PTTPKETAPTTPKGTAPTTLKEP 720
1154 LPMDPKKLAPFSGVKQEQLSRGOAGPPESLG-----VPTAQBASVLRGTALGSPVGGSI 1210
721 APTTPKAP-----KELAPTTPKETSSTSDKAPATTP-----KGTA----- 758
1211 GIPSTRVPSDAITYRGSITHTGTPADVLYKGTITFIIGEDSPSLDRGREDSLPKGHVY 1270
759 -PTT--PKEPAT-----TPKKEPATTPKGTAPTTLKEPATTPKPPAPKELAP----- 804
1271 EGKKGHVLSEYEGMSVTQCSKEDGRSSGPPHETA--APKRTYDMWEGRVGRAISSASIE 1328
805 -----TTTKGPTSTT-----SDKPAPTTPKETAPTTPKKEPATTPKAPATTPPTP-- 850
1329 GLMGRAIPP---ERHSPHLLKEQHIRGSITQGIPTSRVVEAQEDYLRREAKLKREGT- 1384
851 -----PPTTSEVSTPTTPKEPTTIHKSPDESTE-----LSAEPPTPK 887
1385 -----PPPPSRDLTEAYKTQALGPLKPAHEGLVATVKEAGRSIHEIPREBLRHTPE-L 1439
888 ALENSKKEGVTTKT-----PAATKPE--MTTAKD-----KITERDLRTTPTT 931
1440 PLAPRPLKESGIT-----QGTPLKVDTCAS-----TTGSKK 1470
932 TAAPKMTKETATTTETKTESKITATTQTSTTTQDTPPTTKITTLKTLTLPKPVTTTKT 991
1471 HDVRSILGSPGTFPPVHPDVMADARALERACYESLSKRSRPGTASSGGGS-IARGAPVI 1529

992 ITTTEIMNKPEET-----AKPKDRATNSKATTPKPKQPKTKAPKPKPTSTTKPKPT 1039
1530 VPBLGRQPSPLYYEDHGAPFAGHLPRGSPVTWRE--PTPRLOEGSLSSSKASQDRKLT 1587
1040 MPRVRKPKPTT-----TPRKMTSTWPELNPSTRIAEAMLT-----TT 1077
1588 TPREIAKPSHSTVPEHHPHIPISPYEHLRLRGVGD--LYRSHIPLAFDPTSTIPRGIPLD 1644
1078 RPNQ---TPNSKLVE-----VNPKSDAGAGETPHMLLRPHV---FMPEVTP---DMD 1123
1645 AAAAYLPRHLAPN 1658
1124 -----YLPR--VPN 1130

RESULT 17
US-09-854-856-52
; Sequence 52, Application US/09854856
; Patent No. 65411252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 2157
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2157)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-52

Query Match 3.2%; Score 422; DB 4; Length 2157;
Best Local Similarity 19.8%; Pred. No. 1.2e-15;
Matches 513; Conservative 291; Mismatches 943; Indels 844; Gaps 114;

QY 147 PVSPSPPHTDPELELVPPRLSKBELIQNMDRVDREITWVEQIQISKLLKKKQOOLBEEAAK 206
DB 39 PLSLPQPSIPAAPVQSAPEPEPHRETV-----TATATSQVAQPPAAAAPEQAV 89
QY 207 PPEP-----EKVPSPPTIESKHSLSVLIYDENKKAAHRLLEGLPQVELPLY 257
DB 90 GPAPTSPSTSKDRVPSQPSL-----VSGKEPPDA 121
QY 258 NQPSDTROYHENIKINQAMRKLLYFKRRNHARKQWKQFCQRYDQLMEALEKKVERIE 317
DB 122 RSGSG-----GGSAPKEPERSQOQDDI--EELETRAVGMS 155
QY 318 NNPRRRAKESKV--REYEEKQFPEIRKQ-----ELQERMOSRVQORSGLSMSAARSE 369
DB 156 NDGRFLKDFIEIGRGSFKTVYKGLDPTTVEVAVCELODRK-----LTKSERQRP 205
QY 370 HEVSEIIDGSEONLEKQMRQLAVIPMLYDADQORIK-----FINNGLM-ADPMKVYK 424
DB 206 KEEAEMLKGL-QHPNIVR-----FYDSWESTVKGKCCIVLVTMLTSGTLTKYL 253
QY 425 DR-----QVMNWSBQEKETFEKPMQHPK-----NFGLIA 455
DB 254 KRFKWKIKVLRWCQRILKGLQFLHTRTPPIIHRDLKCDNIFITGTVSGVKTGLDGL-- 311
QY 456 SFLEKTVASCVL-----YYLTKQENY-----KSLVRSYRRRGKSOQOQOQO 501

Db 312 ATLKRASFAKSVIGTPEFMAPENYEBKYDESVDVYAFGCMLEMATSETYYPSECQNAQI 371
QY 502 QOQOQOQOOP-----MPRSSQ-----EEDKEKEKEAEKEBEKEDEVENDEKEDLLK 547
Db 372 YRRVTSVGRPASDKVAIPEVKIEIEGCIQONKDERYSIKOLLNHAFFQBEETGVRVELAE 431
QY 548 EKTDDTSGEDNDEKEAVASGRKTANSQGRKRGRITRSMANEANSE-EAITPOQSIAELAS 606
Db 432 E-----DDGEKIAIKLMLRIEDIKIKGKYKDNEAIEFSDFLDRDVPEDVAQ--- 478
QY 607 MELNESSRWTEEBEMETAKGLLEHGRNWSAIAIRMGVSKTVSOCKNFYFVNYKQNLDEIL 666
Db 479 -EMVESGYCEGDKHTMAKAIDR-----VSLIK-----RKREQQLVR 516
QY 667 QQKLMKEKERNARRKKKA-----PAAASEEAAFPVPPVEDEMEASG 709
Db 517 EEOKEKKQEBESSLKQVEQSSASOTGIKQLPSASTGIPTASTTSASVSTQVEEPEA-- 574
QY 710 VSGNEBEMVEEABALHASGNEVPRGCSGPATVN--NSDTEIPSPHTEAAKDTGONGP 767
Db 575 -DQHQLQYQQPSISVLSGTVDSGGQSSVFTESRVSSQQTVSYSQSH-EQAHSTGTVP 632
QY 768 KPPATIGADGPPG--PPT-----PPRTSRAPTEPT-PASEATCAPTPPAPPS 814
Db 633 HIPSTVOAOSQPHGVYPPSPSVQOQIQQTAPPOQTQVYLSQTSSEATTA-----QPV 687
QY 815 PSAPPVVPKKEEKEETAAPPE--EGEBOKPAAEE--LAVDTGKAEBPVKSECTEEA 870
Db 688 QPOAPQVLFQVSAGKQLVSPQVPTTQGEPOIIPVATQPSVVPVHSGAHFLPV----- 739
QY 871 EEGPAKGDAEAAEATAEGALKAEKKEGGGRATTAKSGAPQDSDSSATCSADEVDEAE 930
Db 740 -----GQPLPTPL-----LPQYVPSQIPSTPHYSTAQ 767
QY 931 GGDKNRLLSPRPSLLTPTGDPANASPOKPLDLKQLKQRAAAIP-----PIQVTKVHEP 984
Db 768 TG-----FSLPTTMA-----AGITQPLLTASSATTAAIPGVSTVVPQSULTLLQ 814
QY 985 PREDAAPTRPAPPAPPPQMLQPESDAPQPGSSPRGKRSRAPPADKEAFAEAQKLP 1044
Db 815 VTO-----LPSQVHPQLLOP--AVQSMGI-----PANL-GQAAEVLPLSSG 851
QY 1045 DPPCWTSGLPVPPPREVIKASPHADPSAFSAPPCHPLPLGLHDTARPVL--PRPPTI 1102
Db 852 D--VLXQGPPLPPQY-----PGDSNIAPSSNVASVCIHST---VLXPPMPTEV 896
QY 1103 SNPPPLISSAKHPSV---LEROIGALSQMSVOLHVPYSEHAKAPVGPVTMGLPLPMDPK 1159
Db 897 LATPGYFPTVQVYVESNLLVPMGV--GGQVQVSPGGSLAQAPTSSQAV----- 947
QY 1160 KLAPFSGVKQQLSPRGAQPPESLGV-----PTAQEASVLRGTAIGSVPGGSITKGI 1212
Db 948 -LESTQGV-----SQAAPAEFVAQOQATOPTITLASSV--DSAHSDVASG-MSDG- 994
QY 1213 PSTRVPSDSAITYRSGITHGTADVLKGTITRIIGEDSPSLDRDREGDSLPGKHVIYEG 1272
Db 995 -NENVPSSSG-----RHEGRTTKRHKYKRSVRSRSRHEKTSRPLRLINVS 1038
QY 1273 KGHVLSYEGCMVTOCSKE-----DGRSSSGPPHETAAPKRTYDMEGRVG 1319
Db 1039 NKGD-----RVVECOLETHNRKMVTFKFDLDGN-----PBEIATIMVNDPI----- 1081
QY 1320 RA1SSASIEGLMGRA1PPERHSPHILKEQHHRGSIQTGIPRSVYRAQEDYLRREAKLLK 1379
Db 1082 LALERSFVDQVREII---EKADEMLESDEVSPBEGDGL--ESLQCKDDYIGFSGGQKLE 1136
QY 1380 REGTPPPPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRS--IHEIPREELRHTP 1437
Db 1137 GEFKQPIPASSM-----PQIGIPTSSLTQVHVSAGRRFVSPVPSRSLRESK 1184
QY 1438 ELPLAPRLKEGSIQGTPLKYDTGASTTGSK-----KHVRSI----- 1476
Db 1185 VFP-----SBIT-----DTVAASTAQSPGMNLSHGSASSLSQQAFFSELRRQMTE 1229

QY 1477 -----IGSPCRTLTPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSIARGAP- 1527
Db 1230 GNTAPPNESHGTPTFPVVP-----FLSSIAGVPTTAAATAAPVPATSSPP 1275
QY 1528 -----VIVPELCKPQSP--TYEDHGAPFAGHLPRGSPVTWREPTPRLOEGLSSSKA 1579
Db 1276 NDISTSVIOSEVTVTEEGIAGVATSTGVVTSGL-----PIPPVSESPVUSVV 1325
QY 1580 SQORKLSTPREIA---KSPHSTVPEHHPHIPSPYEHLLRGVSGDLYRSHIPLAFDPTS 1636
Db 1326 SS-----ITIPAVVSISTTSFSLQVPTSTSEIV-----VSSTALYPS----- 1362
QY 1637 IPRGIPLDAAYLYLPHRLAPNPTYPHLYPPVLI-----RGYPDT 1676
Db 1363 ---VTVSATSASAGGSTATPGK-----PPAVVSOQAAGSTTVGATLTSVSTTSPST 1413
QY 1677 AALENRQ-----TIINDYITSQOMHNTATANA-----QRA 1707
Db 1414 ASQLSIQLSSSTSTPTLAETVVVSAHSLDKTSHSSTTGLAFSLASAPSSSSSPGAGVSSYI 1473
QY 1708 DMLRGLSPR-----ESSLALNYAAGPRGIIDLSQVPHLPVLVPTPGTPATAMDLAYL 1761
Db 1474 SQPGLHLPLVIFSIVASTPILPOAGFTSTPLLQVPSIPPLVQPVANVAV---QOTLI 1530
QY 1762 PTAPQPFSSRHSSSPLSPGQP--THLTKTPTTSSSERDRDRDREREKSIILSTTT 1820
Db 1531 HSQOPQ-----ALLPNQPHTHCP-----EVDSDTOPKAPGIDDIKT 1566
QY 1821 VEHAPIWRPGTQSSSGSSSGSSGSSSRPASHAHQHSPISPRTODALQORPSPVLHN 1880
Db 1567 LEE-----KLRSFSEHSSGA-----CHASVLETS-----LVIES 1598
QY 1881 TGMKGI-ITAVESKPTVLRSSTSTSPVPAATFPATHCPLGTLGDGVYPTLMPEVLLP 1939
Db 1599 TVTPGIPTTAVAPSK--LTSIT-----SICLPPTNLPLG----- 1631
QY 1940 KEAPRVARPERPRADTGHAFLAKPPARSGLPEASSPSKSEPRPLVPVPSGHATARTPA 1999
Db 1632 ---TVALPVTVPVTPGVSTPVSTTSGVKPGTAPSKPPLTKAPVLPVGTLPAGTLP 1687
QY 2000 KNLAHHASDPDPAPASADPHREKTQS-KPFSIOEELRSLGYHSGSSSPSGVEPVSP 2058
Db 1688 EQ-----PPFPGSL-----TOSQOPLLEDLDAQLR-----RTLSPXITVTS 1726
QY 2059 VSSPSLTHDKGLPKHLELDKSHLEGELRPQGPVKLGGEAAHPLRLPPE---SOPS 2115
Db 1727 V-----GPVSMMAPTA--ITEAGTOPKQGVSOVK 1753
QY 2116 SSPLLQTAQV-----KGHQRVVVTLAQHISEVITQDYTRHHPOQLSAPLAPLYSFPQASC 2171
Db 1754 EGPVLATSSGAGVFKMGRFQVSVAA-----DGAQKEGKNKSEDAKSVHFESSTSES 1804
QY 2172 PVLDLRRPPSDLYLPPP-----DHGAPARGSPHSEGGKRSPEPNKTS----- 2213
Db 1805 SVLSSSSPESTLVKPFNGITIPGISSDVPESAHTKTASEAKSDTQOPTQVGRFQVTTA 1864
QY 2214 -----VLGGGEDIB-----PVSPPEGMTEPHSRSVAVPLLYRDEGOTEPSRMGSKS 2261
Db 1865 NKVGRFSVKTEDKITDTTKKEGVPVSPFMDLEQAVLPAVPIKKEP-ELSEFSLN--- 1920
QY 2262 PGNTSQP-PAFFSKLTESAMVKSKQKQINKNLTHNRNEPEYNISQPGTEIFNMPAIT 2320
Db 1921 -GFSSDPEAAFLSRDVGDCSGSPHSFHQLSSKSL-----PSQNLSQLSNSFNSSYMS 1972
QY 2321 GTGLMYRQAVO-----EHASTMGLEAIIRKALMKYDQWEESPPLSANAFPLN 2372
Db 1973 SDNESIEDLLELRLRLDKHLKEIQDLQSQKHEIESLYTKLGKVP----- 2022
QY 2373 ASASLPAAMPITAADGRSDHLLTSPGGGKAKYSGRPSRRKAKSP-APGLASGDRPPSV- 2430
Db 2023 -AVIIPPAAPLS---GRRRRPTKS-----KGSKSSRSSSLGNKSPQLSGNLSQQAASVL 2073

QY	2431	---SSVHSEGD 2438		QY	607	MELNESSRWTEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYNYKQKNLDEIL 666
Db	2074	HPQOTLHPGN 2084		Db	539	-EMVESGYVCEGDHKTAKIKDR-----VSLIK-----RKREQQLVR 576
RESULT 18						
US-09-854-856-20						
; Sequence 20, Application US/09854856						
; Patent No. 6541252						
; GENERAL INFORMATION:						
; APPLICANT: Walke, D. Wade						
; APPLICANT: Hilbun, Erin						
; APPLICANT: Donoho, Gregory						
; APPLICANT: Turner, C. Alexander Jr.						
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides						
; TITLE OF INVENTION: Encoding the Same						
; FILE REFERENCE: LEX-0178-USA						
; CURRENT APPLICATION NUMBER: US/09/854,856						
; CURRENT FILING DATE: 2001-05-14						
; PRIOR APPLICATION NUMBER: US 60/206,015						
; PRIOR FILING DATE: 2000-05-19						
; NUMBER OF SEQ ID NOS: 64						
; SOFTWARE: FastSeq for Windows Version 4.0						
; SEQ ID NO 20						
; LENGTH: 2217						
; TYPE: PRT						
; ORGANISM: Homo sapiens						
; FEATURE:						
; NAME/KEY: VARIANT						
; LOCATION: (1)...(2217)						
; OTHER INFORMATION: Xaa = Any Amino Acid						
US-09-854-856-20						
Query Match 3.2%; Score 422; DB 4; Length 2217;						
Best Local Similarity 19.8%; Pred. No. 1.3e-15;						
Matches 513; Conservative 291; Mismatches 943; Indels 844; Gaps 114;						
QY	147	PVSPSPPTDPELELVPPRLSKEELIQNMDRVDRITVVEQIQSKKKQQQLREAAK 206		QY	1045	DPCCWTSGLPPVPVPREVIKASPHADPSAFYAPPGHPLPLGLDHTARPVL--PRPPTI 1102
Db	99	PLSLPQSPAAVPQAPPEPREEV-----TATATSOVAQPPAAAPGEQAVA 149		Db	912	D--VLVYQGFPPPLPQY-----PGDSNIASSNVASVCIHST---VLXPPMPTEV 956
QY	207	PPPE-----EKVPSPPIESKHSRLVQIIYDENRKAEEAHRILEGLGQVELPLY 257		QY	1103	SNPPPLISAKHPV--LEROIGAISQMSVOLHVHYSEHAKAPGVPTMGLPLPMDPK 1159
Db	150	GPAPSTVPSTSKDRVPSPL-----VGSKEPPPA 181		Db	957	LATPGVFPTVQPVYESNLLVPMGV--GGQVQVSPQGGSLAQAPTTSQQAV----- 1007
QY	258	NQPSDTROYHENIKINQAKKLLIFKRNHARKQWKFCORYDOLMEALEKKVERIE 317		QY	1160	KLAPSGYKQEQLSRPGAGPPESLGV-----PTAQEASVLRGTALSGVPGSGITKGI 1212
Db	182	RSGSG-----GGSAKEPQBERSQQDDI--EELETKAAGMS 215		Db	1008	-LESTQGV-----SQVAPAEPAVAQPAQTPTTLASSV--DSAHSDVASG-MSDG- 1054
QY	318	NNPRRAKESKV-REYVEKQFPBIRKQ-----ELQERMQRVQGRGSLSMSAARSE 369		QY	1213	PSTRVPSDAITYRGSITHTPADVLYKGTITRIIGEDSPSLDRGREDSLPKGHVIRG 1272
Db	216	NDGRFLKFDEIGRGSFKTVYKGLDTETTVAVAWCELDQK-----LTKSERQRF 265		Db	1055	-NENVPSSG-----RHEGRTTKHYRKSVRSRHREKTSRKLRLNVS 1098
QY	370	HEVSEIIDLSEQENLEKQMRQLAVIPMLYDADQRIK-----FINNGLM-ADPMKVYK 424		QY	1273	KKGHLVSYEGGMSVTCOSKE-----DGRSSGPPHETRAAPKRTYDMMEGRVG 1319
Db	266	KEBAEMLKGL-QHPNIVR-----FYDSWESVTKGKCVLVLTEIMTSGTLKTYL 313		Db	1099	NKGD-----RVVECOLETHNRKMVTFKFDLDGN-----PEEATIMVNNDFI----- 1141
QY	425	DR-----QVMNWSQEKETTFREKFMQHPK-----NFGLIA 455		QY	1320	RAISSASIEGLMGRAPPEHSPHILKEQHHRIGSITQIGIPRSYVEAOBYLREAKLK 1379
Db	314	KRFKVMKIKVLRSWCRQLKGLQFLHTRTPPIIHRDLKCDNIIFITGTSVKIGDLGL-- 371		Db	1142	LAIERESFVDQVREII---EKADEMLSEDVSVVEPDQGL--ESLOCKDDYGFSGSKLE 1196
QY	456	SFLERKTVAECVL-----YYLTGKNENY-----KSLVRSYRRRKGSKQQQQQQQ 501		QY	1380	RSGTTPPPPPSRLTEAYKTQALGPLKPAHEGLVATVKEAGRS--IHEIPREELRHTP 1437
Db	372	ATLKRAFAKSVIGTFEFMAPEMYEYKDESVDVAFGCMLEWATSEYFSECQNAQI 431		Db	1197	GEFKQIPASSM-----PQOIGIPTSSLTQVVHSAGRRRIVSPVESRLRESK 1244
QY	502	QOQOQOQOQO-----MPRSSQ-----EEKDEKEKEAEBEKEPEVENKEDDLK 547		QY	1438	ELPLAPRLKEGSIQTGTPKYDTGASTGSK-----KHDVRSI----- 1476
Db	432	YRRVTSQVKDPAFDKVAIPVEKEIIEGCIQNKNDERYSIKDLNHAFFQETQVRVELAE 491		Db	1245	VFP-----SEIT-----DTVAATAQSPGMNLSHASLSLQQAFASELRAQMT 1289
QY	548	EKTDDTSGEDNDEKAVASGRKTANSQGRKGRITRSMANEANSE-EAITPOOSAEAS 606		QY	1477	-----IGSCRTPPPVHPLDVMDARALERACVEESLKRPGTASSGSGIARGAP- 1527
Db	492	E-----DDGEKTAIKLWLRIEDIKKLGKYKDNEAIEFSFLDERVDPEDVAQ--- 538		Db	1290	GENTAPPNESHGTPTPPVVP-----FLSSIAGVPTTAATAVPATSSPP 1335
QY				QY	1528	-----VIVPELCKPRQSPL--TYEDHGAPFAGHLPRGSFVTMREPTPLRQESLSSKA 1579
Db				Db	1336	NDISTSVIQEVVPTVEGIAGVATSTGVVTSGL-----PIPPVSESPVLSSVV 1385
QY				QY	1580	SQDKLTSTPREIA---KSPHSTVPEHHPHSPYEHLLRGVSGVDLYRSHIPLADPTS 1636

; PRIOR FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 18
 ; LENGTH: 2354
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)...(2354)
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 US-09-854-856-18

Query Match 3.2%; Score 422; DB 4; Length 2354;
 Best Local Similarity 19.8%; Pred. No. 1.4e-15;
 Matches 513; Conservative 291; Mismatches 943; Indels 844; Gaps 114;

QY	147	PVSPPPPHDTELELVPRRLSKKEELIQMDVRDREITVWQOISKLKKKQOQLEEEAAK	206
DB	99	PLSLPQPSIAA VPOSAPPEHRETV-----TATATSOVAQPPAAAAAEGEQA	149
QY	207	PPRP-----EKPVSPPPTESKHSRLVQIYDENKKAEAAHRILEGPGQVPELPLY	257
DB	150	GPASTVPSTSKDRVSPQSL-----VGSKEEPPPA	181
QY	258	NQPSDTRQYHENIKINQAMRKLLIYFKRRNNHARKQKFCORYDQLEALEKKVERIE	317
DB	182	RSQSG-----GGSKEPEQERSQQDDI-ELETKAVGMS	215
QY	318	NNPRRAKESKV-REYEEKQFPEIRKQR-----ELERMQSRVQRGSGLSMSAARSE	369
DB	216	NDGRFLKFDIEIGRSFKTVYKGLDTETTVAVWCELQDRK-----LTKSERQRF	265
QY	370	HEVSEIIDGLSQENLEKQMRQLAVIPMLYDADQORIK-----FINMNGLM-ADPMKVYK	424
DB	266	KEEAEMLKGL-QHPNIVR-----FYDSWESTVKGKCVILVTELMTSGTLKTYL	313
QY	425	DR-----QVMNWSSEQKETEFREKFMQHPK-----NFGLIA	455
DB	314	KRFKVMKIKVLRSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSKVIGDLGL	371
QY	456	SFLERTVAECVL-----YYLTKGNENY-----KSLVRSYRRRGSKSQOQQOQQ	501
DB	372	ATLKRAFPKSVIGTPEFNAPMEYBEKYDESVDVYAFQMCLEMATSEYPYSECQNAQI	431
QY	502	QOQOQOQOOP-----MPSRQO-----BEKDEKEKEAEKEEKEPEVENDKEDLLK	547
DB	432	YRVTVSGVPASFDKVAIPEVKEIEIGCIROKNKDBRYSIKOLLNHAFFQETGVRVELAE	491
QY	548	EKTDDTSGEDNDEKEAVASGKRKTANSQORRRGRITRSMANEANSE-EAITPQOSAELAS	606
DB	492	E-----DDEGKIAIKLWRIEDIKLKGKYKDNEAIEFSPDLERDVEDVAQ----	538
QY	607	MELNESSRWTEEMETAKGELLEHGRNWSAIARMVGSKTVCQKNFYNYKKQNLDEIL	666
DB	539	EWESGYVCEGDHKTMAKAIKDR-----VSLIK-----RKREQQLVR	576
QY	667	QQHLKWEKERNARKKKA-----PAAASEEAAFPVVEDEMEASG	709
DB	577	EOEKKKQOESSLUKQVQESSASQTGIQLPSASTGIPTASTTSASVSTQVEPEPEA--	634
QY	710	VSGNEEMVEEAEALHASGNEVPRGECSPATVN--NSSDTESIPSPHTEAAKDTQNGP	767
DB	635	-DOHQOLYQOQPSISVLSDGTVDGSGSVFTESRVSSQOIVSYGSOH-EQAHSTGTVPG	692
QY	768	KPATLGAQDPPPG--PPT-----PPRRTSRAPIEPT-PASEATGAPTPPPAPPS	814
DB	693	HIPSTVQAQSPGHVYVPPSSVQOQIQQTAPPQOITVQYLSQTSQTSSEATTA-----QPVS	747
QY	815	PSNPPVPVPEKEEBETAAPVPE--EGEOKPPAAEE--LAVDTGKAEPEVKSECTEEA	870
DB	748	QPOAQOVLPOVSAGKQLPVSPQVPTIQBEPQIPVATQPSVVPVHSGAHFLEV-----	799

Mon Apr 19 08:15:00 2004

[illegible]

RESULT 21

```

US-07-757-022B-142
; Sequence 142, Application US/07757022B
; Patent No. 6433142
;
; GENERAL INFORMATION:
;
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine M.
; APPLICANT: Hewick, Rodney M.
;
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
;
; ZIP: 02140
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07757.022B

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Mon Apr 19 08:15:00 2004

Qy	1129	MSVOLHVPYSEHAKAP-----VGPVTMGLPLPMDPKKLAPFSGVKQOLSPRCQAGPPPS	1183
Db	648	-----PTTPKETAPTPKGTAPPTLLKEKAPPTPKKAP-----KELAPTTTKKEPTST	694
Qy	1184	LG--VPTAQEASVLRGTALGSPVGGSIITKGIPSTRVPSDSAITYRGSITHGTFADVLK	1240
Db	695	TSDKPAPPTP-----KGTA-----PTT--PKEPAT-----TPKEPATTPK	729
Qy	1241	GTITRIIGEDSPSRDLRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTCQSKEDGRSSGP	1300
Db	730	GTAFTLLKEKAPPTPKKAPKELAP-----TTTKGPTST-----SDKDAPTT	772
Qy	1301	PHEFA--APKRYTDMGRVGRVRAISSASIEGLMGRAIPP--ERHSPHLKEQHHRGSI	1355
Db	773	PKETAPTPKEPAPTPPKKAPPTPETP-----PPTTSEVSTPTTTKEPPTTHKSP	823
Qy	1356	TQGTIPRSVIAQEDYLRREKLLKREGTP-----PPPPSRDLTEAYKTQALGPLKLKPA	1410
Db	824	DESTPE-----LSAEPPTKALENSPKBGPVTKT-----PAATKPE	860
Qy	1411	HEGLVATVKEAGRSIHEIPREELRHTE--LPLAPRLKEGSIT-----	1452
Db	861	-----MTTAKD-----KTTREDLATPTTTTAAFKMTKETATTTEKTESKITATTTQVT	911
Qy	1453	-----QGTPLYKDTGAS-----TTGSKKHDSVLSLIGSPQRTFPFVHPLDVMADARALE	1500
Db	912	STTTQDTPFPKITLLKTTLLAPKVVTTTKTTTITTEIMNKPET-----AKPKD	959
Qy	1501	RACEYESLKSRCPTASSGGGS--IARGAPVIVPELKGKRSQSPLTIEDHGCAFPAGHLPRGSP	1559
Db	960	RATNSKATTPKQKPTKAPKXPTSTKKPKTMPRVRKKPTTP-----TPRKMT	1006
Qy	1560	VTMRB--PTPLROEGSLSS--KASORDKLT-----STPREIAKSPHSTV	1600
Db	1007	STMPENPSTRIAENMLQTTTRPNTGPNPSKLVENVNPKSDAGGAEGETPHMLLR--PHVFM	1065
Qy	1601	PEHHPH-----PISPYEHLRLGVSVDLYRSHIPLAFLDFTSIPIRGIPLD	1644
Db	1066	BEVTQDMNYLPRVPPNQGIIIN-----PMLSDETNINCNGKPDV	1102

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RESULT 23
US-07-757-0022B-50
US-07-757-0022B-50
Sequence 50, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:

```

[illegible]

Db 608 -PTTKETAPTTPKGTAPTTLKEPAPTTPKKPAP-----KELAPTTTKEPTSTTSKPA 660
QY 1187 PTAQASVLKRGALGVSGSITKGIPTSTRVPSDSAITVYRGSITHGTGTPADVLKGTITRI 1246
Db 661 PTP-----KGTA-----PTT--PKAPAT--TPKEPAPTTPKGTAPT 695
QY 1247 IGEDSPRLDRGREDLSLPGKHVIYEGKGHVLSEYEGMSVTQCSKEDGRSSGPPHETA- 1305
Db 696 LKEPAPTTPKKAPKELAP-----TTTKGTSTT-----SDKPAPTTPKETAP 738
QY 1306 -APKTYDMMEGRVGRGAISSASIEGLMGRAP--ERHSPHLKEQHHRGSIQTGIPR 1361
Db 739 TTPKEPAPTTPKKAPATTETP-----PTTSEVSTPTTKEPTTIHKSPDESTPE 789
QY 1362 SYVEAQEDYLRREAKLLKEGT-----PPPPSRDLTEAYKTQALGPLKLPAPHEGLVA 1416
Db 790 -----LSAETPKALENSPKFVPTTKT-----PAATKPE---MTT 823
QY 1417 TVKEAGRSIHIEPRELHTPE-LPLAPRLKEGSIT-----O 1453
Db 824 TAKD-----KTVERDLRTPTTTAAPKMTKETATTTKTTESKITATTQVTSSTTQD 877
QY 1454 GYPLKYDTGAS-----TTGSKKHVRSILGSPGRTFPVPHLDVMDARALERACYEE 1506
Db 878 TTFPKITLTKTTTLAPKVTITTKTITTTIMNKPEET-----AKPKDRATNSK 925
QY 1507 SLKSRPGCTASSGGS-IARGAPVIVPELKGPROSLTYEDHGAPFAGHLPRGSPVTMRE- 1564
Db 926 ATTPKQOKTKAPKKTSTSKPKTMRVRKPKTTP-----TPKMTSTWPEL 972
QY 1565 -PTPLQEGSLSS--KASQDRKLT-----STPREIAKSPHSTVPSHHPH 1606
Db 973 NPTSRIAEAMLQTTTRNPNTNSKLVNPKSBDAGAGETPHMLLR-PHFVMPSEVTPD 1031
QY 1607 -----PISPEHLLRGVGVLDYRSHIPLAPDPTSIIRGPILD 1644
Db 1032 MDYLRVPVNGIIN-----PMLSDETNICNGRPVD 1062

RESULT 24

US-07-757-022B-58
; Sequence 58, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,022B
; FILING DATE: 19910910
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1049 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-757-022B-58

Query Match 3.2%; Score 416.5; DB 4; Length 1049;
Best Local Similarity 21.2%; Pred. No. 1e-15;
Matches 264; Conservative 128; Mismatches 503; Indels 349; Gaps 56;

QY 495 QQQQQQQQQQQQQQQQQMPRSSOEKDEKEKEKEAEKE-EEXPEVENDKEDLLKEK----- 549
Db 65 EEHSVSSENQESSSSSSSSSSSTIWKIKSKNSAANRELQKLVKDNKKNRTKKKPTK 124
QY 550 ---TDDT-SGENDKEAVASKRKTANSQGRKRGITRSMANEANSEEAITP-QQSAEL 604
Db 125 PVVDEAGSLDNGDPKVTTPDTSTTQHNVSTSPKIT--TAKPINRPSLSPNSDTSKE 182
QY 605 ASMELNNESSRWTEEMETAKGLLEHGRNWSALARMVGSKTVSQCKQNFYNYKKRQNLDE 664
Db 183 TSLTVNKTETVETKETTNTNKQTSIDGKEKTSKETSQIEKTSADL-----APTSK 235
QY 665 ILQOHKLKME---KERNARRKKKAPAAASEEAFPPVVEDEEMEASGVSGNEEEMVEEA 721
Db 236 VLAKPTPKAETTTKGPALTTPKEPTTTPKEPASTTP----- 272
QY 722 EALHASGNEVPRGECSPATVNNSSDTSIESPHTEAAKDTGQNGKPKPATILGADGPPPG 781
Db 273 -----KEPT-----PTTIKSAPTTPKEPAPTTPKSAPTTPKEPAPTTP--KEPA 314
QY 782 PPTPPTTSRAPLEPTPASEATCAPTP--PAPPSAPSAPPVVPKEKEEETAAAPVVEE 839
Db 315 PTPKEPAPTTPKEPAPTTP--TKSAPTTPKEPAPTTPKKEPAPTTPKE--PAPTTPKEPTPT 371
QY 840 GBEQKPPAAEELAVDTGKAEEPVKSECTBEAEEGPAKGDAAEAATAEGALKAEKKEGG 899
Db 372 TPKEPAPTTPKEPAPTTPKEPAPT-----APKKPAPTTPKEPAPTTPKEPAPTTPKKE-- 422
QY 900 SGRATTAKSSGAPQSDSSATCSADEVDEAGDDKRLSPRPSLLTPTGDPANASPOK 959
Db 423 --PSPTTPKEPAPTTPKSAPTTPKEP-----APTTSKAPTTPKE 460
QY 960 PLDLKQLKQRAAAIPIQVTKVHEP-----PREDA--APTKEPAPPAPPQNLQESDAPQ 1013
Db 461 P-----SPTTKEPAPTTPKEPAPTTPKKEPAPTTPKEPAPTTPKEPAPTTPKEPAPT 504
QY 1014 QFGSSPRGKSRSPAPPADKEAFAAEAQKLPGDPP-----CWTSGLPFPVPPREVIKASPHA 1069
Db 505 TTKKPAPTAPKEPAPTTPKETAPTTPKLTPTTPEKLAPTTPKEPAPTTPPEELAPTTEE 564
QY 1070 PDPSAFSAPPQGHPLPLGLHDTARPVLPPTTISNP-PPLISSAKHPSVLIERIGAISQ 1128
Db 565 PTPPT-----PEEPAPT--TFKAAAPNTPKAPAPTTPKEPAPTTPKEPAPTTPKEPA----- 606
QY 1129 MSVQLHVPVYSEHAKP-----VGPVTMGLPLMDPKLAPFSGVKOEQLSPRQAGPPES 1183
Db 607 -----PTTPKETAPTTPKGTAPTTPKKEPAPTTPKKEPAPTTPKKEPAPTTPKKEPAPT 653
QY 1184 LG---VPTAQEASVLKRGALGVSGSITKGIPTSTRVPSDSAITVYRGSITHGTGTPADVLK 1240

Db 654 TSDKAPPTT-----KGTA-----PTT--PKEAPT-----TPKEAPTTPK 688
Qy 1241 GYITRIIGDSRDLRGREDISLPKHGVIYEGKGVLSYEGGMSVTCQSKEDGRSSGP 1300
Db 689 GYATPTLKAPAPTTPKPAKELAP-----TTTGTSTT-----SDKAPT 731
Qy 1301 PHETA--APKRTVDMMEGRVAGRAISSAIEGLMGAIPP---ERHSPHLKEQHHRGSI 1355
Db 732 PHETAPTTKEAPTTPKPAPTTPTP-----PTTSEVSTPTTKEPTTIHKSP 782
Qy 1356 TQICPRSYVEAQEDYLRLREAKLKRGT-----PPPPSRDLTAYKQALGPLKLKPA 1410
Db 783 DESTPE-----LSAEPKALENSPKRGVPTTKT-----PAATKDE 819
Qy 1411 HGLVATVKEAGRSIHEIPRELHRTPE-LPLAPRLKEGSIT-----1452
Db 820 ---MTTAKD-----KTERDLRTPTTTAAPKMTKETATTEKTESKITATTQVT 870
Qy 1453 -----QGTPLKYDTGAS-----TTGSKKHVRSLLIGSPGRFTFPVHPLDVMADARALE 1500
Db 871 STTTQDTTFFKTLITLITLAPKVTTKTITITTEIMNKPEET-----AKPKD 918
Qy 1501 RACYESLSRSPGTASSGGS-IARGAPVIVPELGKPROSPLYEDHGAPFAGHLPRGSP 1559
Db 919 RATNSKATTPKPKPTKAPKPTSTTKPKTPRVRKPTTP-----TPRKMT 965
Qy 1560 VTMRE--PTPRLOGBSLSSKASQDRKLTSTPREIAKSPHSTVPEHHHPISPYEHLRG 1617
Db 966 STMPELNPTSRIAEAMLQT-----TTRPNQ---TPNSKLVE-----VNPKSDAGG 1008
Qy 1618 VSGVD---LYRSHIPLAFDPTSPRGIPLDAAAAYVLPRLAPN 1658
Db 1009 AEGETHMLLRPHV---FMPEVTP---DMD-----YLPR--VPN 1039

RESULT 25

US-07-757-022B-44
Sequence 44, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Geesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patencin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:

Query Match 3.1%; Score 410; DB 4; Length 1270;
Best Local Similarity 21.0%; Pred. No. 3e-15;
Matches 262; Conservative 128; Mismatches 489; Indels 368; Gaps 54;
US-07-757-022B-44

Qy 515 SSOE-----EKDEKEKEAEKEEK-----PEVNDKEDLLKEK----- 549
Db 23 SSOELSCGRCPESFERGECDCDAQCKYDKCCPDYSEFCAEVKDNKNRTKKPTPKP 82
Qy 550 --TDDT--SGEDNDEKEAVASKGRKTANSQGRKGRITRSMANEANSEEAITP-QQSAELA 605
Db 83 PVVDEAGSLNDGDFKVITPDTSTTQHNKVSPTKIT--TAKPINRPSLPNSDTSKET 140
Qy 606 SMELNESSRWTEEMETAKGLLEHGRNWSAIFARVMGKTSVCQKQFNFYKKRQNLDEI 565
Db 141 SLTVNKETTVETKTTTNNKQTSQKKTTSKAKTQSIKTSKDL-----APTSKV 193
Qy 666 LOQHLKWE---KERNARRKKKAPAAASEEAFPPVVEDEERMEASGVSGNEEMVEEAE 722
Db 194 LAKTPKAETTTKGPAALTPPKETPTTPKPEASTTP-----229
Qy 723 ALHASGNEVPRGCSGPATVNNSSDTEIPSPHTEAAKDTGQNGPKPPATLGAQDPPGP 782
Db 230 -----PITIKAAPTTPKEPATTTTKSAPTTPKPEAPTTP-----KEPAP 272
Qy 783 PTPPRTSRAPTEPTPASEATCAPTP--PAPPSAPPPVPVVKKEKEBEETAAAPVVEG 840
Db 273 TTPKEPATTTTKEPATTT-TKSAPTTPKEPATTPKPAPTTPKE--PAPTTPKEPTPT 329
Qy 841 EBQKPPAAELAVDTGKAEPVKSECTEAEAGPKAGKDAEAAEATAEGALKAKEKESGS 900
Db 330 PKEPATTPKEPATTPKEPATTP-----APKPAPTTPKEPATTPKPEAPTTPKE-- 379
Qy 901 GRATTAKSSGAPQSDSSATCSADEVDEAGGDKNRLLSRPSLLTPTGDPANASPKPQ 960
Db 380 -PSPTTPKEPATTTTKSAPTTTKEP-----APTTKSAPTTPKEP 418
Qy 961 LQLKQLKQRAAAIPIQVTKVHEP-----PRED--APTKEPATTPPPQNLOPESAPQ 1014
Db 419 -----SPTTKEPATTPKPEPATTPKPAPTTPKPEPATTPKPEPATTP 462
Qy 1015 PGSSPRGKSRPAPPADKFAFAEAQKLPDGP-----CWTSGLPFPVPPREVIKASPHAP 1070
Db 463 TKKPAPTAPKEPATTPKETAFTTPKLTPTTPEKLAFTTPKEPATTPPEELAPTTPEP 522
Qy 1071 DFSAFSYAPPGHPLPLGLHDTARVLPRTPTISNP--PPLISSAKHPSVLIERQIGASQGM 1129
Db 523 TPTT-----PEEPAPT-TPKAAAPNTPKPEPATTPKPEPATTPKPEA----- 563
Qy 1130 SVQLHVPVSEHAKAP-----VGPVTMGLPLPMDPKLAPFSGVKQBLSPRGQAGPPESL 1184
Db 564 -----PTTPKETAPTTPKGTAPTTLKPEPATTPKPEPATTP-----KELAPTTTKEPTST 611
Qy 1185 G---VPTAQEASVLRGTALGVSFVGSIITKGIPSTRVPSDAITYRGSITHTGPADVLK 1241
Db 612 SDKPAPTTP-----KGTA-----PTT--PKEAPT-----TPKEPATTPKG 646

Db 1205 S-----TISPFSSNEEDKFRSALRDAYCSEVKASTTLDIKDISAVSSSEKVSF--SKSPS 1258
QY 1182 ESIGVPTAQEASVLRGTALGSPVGGSIITKGIPTSRVPSDAITYRGSITHGTPADVLYKG 1241
Db 1259 LSPSP-----SPLEKTPJGE-----RSVNFSLTPNEIKVSAEAVAPVSP-----1300
QY 1242 TITRIIGEDPSRLDRGREDSLPKGHVIEYEGKKGHVLSYEGGMSVTCQSKEDGRSSSGPP 1301
Db 1301 VTQEVVEHCASPEDKLEVVSPQSV--TGSAGHTPPYQ-----SPTDEKSSHLPT 1350
QY 1302 HETAAPKRTYDMMGRVGRRAISSASIEGLMGRAPRPHRSPHLKBQHHRIGSITQGIPIR 1361
Db 1351 EVIEKPP-----AVP-----VSF 1363
QY 1362 SYVEAQEDYLREAKLLKEGTPPPPPSRDLTEAYKTOALGPKLKP-----AHEG-L 1414
Db 1364 EFSDAKDN-----ERASVPMDEPVD--SEPIEKVLSPLRPPPLIGESAYESFL 1414
QY 1415 VATVKEAGRSIHIEIPRELRHTPELAPRPL-----KEGSITQGTPLKYDTG 1462
Db 1415 SADDKASGRGA--ESPFEKSGKQSPDOVSPVSEMTSTSLYQDKQBGKSTDFAPIKEDFG 1473
QY 1463 ASTTGSKKHVRSLLIOSPG-----RTFPPVHP--LDVM-----AD 1495
Db 1474 QE---KKTDDVEAMSSQPALALDERKLGDVSPQTQIDVQSGFKEDTKMSISEGTVSDKS 1530
QY 1496 ARALERACEESLKSPPGTASSGGGIARGAVIVPELCKPRQSPPLTYEDHGAPAGHLP 1555
Db 1531 ATPVDEGVADYVSHMEGVASVSTAVTSS---FPEPTDDVSPBLHAEVSPSHSTVED 1587
QY 1556 RGSPTVMRPTPRLOEGSLSSSKASQDRKLSTPREI-----AKSPHSTVPEHHPHIPISPY 1611
Db 1588 DLSLSVVQPTPTTFQETESPSKECPWMSISPPDFSPKTAKS--RTPVQDHRSE-----1641
QY 1612 EHLRGVGVDLVRSHIPLAFDPTSIPRGIPLDAAAYVLRPHLANPYPHYPPYLIR 1671
Db 1642 -----QSSMSIEFGQESPEQSLAMDFS-----RQSPDHPVT-----1672
QY 1672 GYPDTAALENROTIINDYITSQMHNTATAMAQRADMLRGLSPRESSIALNVAAGPRGI 1731
Db 1673 GAGVLHITENGPTFV--DYGFSDM-----QDSLSHKIPPMEEP---STQDN-----1715
QY 1732 IDLSQVPHLPVLVPTPGTATAMDRLAYLTAPOPFSSRHS-----SSPLSPGGPHTLTK 1787
Db 1716 -DLSEL-----ISVSQVEASPST-----SSAHTPSQIASPLQEDTLDSDVAP 1755
QY 1788 PTTTS-----SSRERDRDRDRDREREKSLTSTTVEHAPIWRPGTEQSGSGSGSG 1842
Db 1756 PRDMSLYASLTSKQVQSLGE-----KLSPKSDISPLTPRESSPLGYFTFSDSTSAVKET 1811
QY 1843 GGGGSSSRPASHAHQHSPISPRTOALQQRSPVLHNTGMKGIITAVBSPKPTVLRSTS 1902
Db 1812 ATCHSSSP-----PIDAASAEYGFVFRASVLFDTWQHHLALNRDLSTPGLKDSG 1861
QY 1903 TSSFVRPAATFPFATHCPGLGTLGTVYPTLMEVLLPKEA-----1942
Db 1862 GKTF-----GDFSVAQKPEETTRSPDEEDYSEYKTRTSDVGGYV 1905
QY 1943 -PRVAPERPRADTGAF--LAKPPARSGLEPASSKSEPRPLVPVPSGHATARTPA 1999
Db 1906 YEKIERTKSPSDSGSYETIGK-----TTKTPEDGDGYSEIIEKTT-----RTPE 1951
QY 2000 KNLAPHASDPAPPASADPHREKTOSKPFPSIOELRSLGYHGSSYSPEGEVPSVPV 2059
Db 1952 EGGYSYDISEKTSPP--EVSQYSEYKTERSRLLDDI---SNGYDDSE---DG-----1997
QY 2060 SSPSLTHDKLPHLBEKSHLEGSLRKPQKQGVKLGGEAAHLRPLRPESQPSSSL 2119
Db 1998 -----GHTLGDPSYSYETTEK-----ITGFPESEGYSS---2024
QY 2120 LQTAPGVKGHQRVVVTLAQHISEVITQDTRHHHQOLSAPLPAPLYSPFGASCCEVLDLRP 2179
Db 2025 YETSTKTRTPDSTYCYETAETKTRT-----PQ-----ASTYSYETSDLCYTAEKKS 2072
QY 2180 PSDL-----YLPDPDHGAPARGSPHSGRSPSPNKTSLVGGGEDGIEPVS 2226
Db 2073 PSEARQDVLDCLVSSCEYKHPKTELSPSFINPPLWFSEBTESESEKPLTQSGGAP--2130
QY 2227 PPEGMTPECHRSRVAVPLLYRDGEOTEPSRMGSKSPGNTSQ--PPAFFSKLTESNSAMVK 2284
Db 2131 PPGGKQGG-----RQCDTPTPTSVSESAPSQTDSDVPE-----TE-----2167
QY 2285 SKQBIINKKLATHNREPEYNISQPGTEIFNMPAITGTGLMTYRSQ-----AVQE-----2334
Db 2168 -ECPISITADANIDSESE-----TPTDKTVTYKMDPPPPVQQRSPSP 2212
QY 2335 -HASTNM-----GLEAIIRKALMGKYDQWEESSPLSANAENPLNASASLPAAMPITAAD 2387
Db 2213 RHPDVSMVDPEALAEQNLKAL--KKDKKKT-----KTKKPGTKTKSSSPVKKSD 2262
QY 2388 GRSDHTLTPSGGGGKAKVS---GRPSSRKAKSPAGCLASGDRPPSVSVHSEGDGNCRRTP 2444
Db 2263 GKSKPLAASPKPAGLKESSDKSVRSVASPKKESVEKAAKPTTTTPEVKAARGEKDKETKN 2322
QY 2445 LTRVWEDRPSAGSTPPFPNPLIMLQAGVMASPPPGCLPAGSGPLAGPHHA 2497
Db 2323 AANASAKSATATAGP-----GTTKTKSSAVPPGLPVLDLCYIPNHS 2367

RESULT 27
US-07-757-022B-74
; Sequence 74, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,022B
; FILING DATE: 19910910
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseir, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: G1 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851

INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 1038 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-74

Query Match 3.1%; Score 408.5; DB 4; Length 1038;
Best Local Similarity 21.0%; Pred. No. 2.9e-15;
Matches 272; Conservative 133; Mismatches 497; Indels 395; Gaps 58;

515 SSQE-----EKDKKEKEAEKEEK-----PVENDKEDLLKEK-----549
Db 23 SSQELSGKGRCFESFERGECDCDAQCKYDKCCPDYSEFCAEVGNKNNKRTKKPTPKP 82

550 --TDDT--SGEDNDEKAVASKGRKANSQGRKGRITRSMANEANSEEAITP--QQSAELA 605
Db 83 PVVDEAGSLDNGDFKVTTPDSTTQHNKVSTSPKIT--TAKDINPRPSLPFNSDTSKET 140

606 SMELNESSRWTEEMETAKGLLEHGRNNSAIARMVSKTVSOCKNFYFNYKKRONLDEI 665
Db 141 SLTVNKETTVETKETTNNKQSTGDKKETSASAKTQSEKTSKADL-----APTSKV 193

666 LQHKLKME---KERNARRKKKAPAAASEEAAPPVVEDEMEASGVSGNEBEMVEAE 722
Db 194 LAKPTPKAETTTKGPALTTPKEPTTPPKEPASTTP-----229

723 ALHASGNEVPRGSCGPAIVNNSDYESIPSPHTEAAKDTGQNGPKPPATLGADGPPGP 782
Db 230 -----KEPT-----PTTIKSAPTTPKEPAPTTTSAPTTPKEPAPTTT-----KEPAP 272

783 PTPPRTSRAPIBPTPASEATGAPTP--PAPPSAPPPVVPKPEKEEETAAAPVVEEG 840
Db 273 TTPKEPAPTTTKEPAPTT--TKSAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTT 329

841 BEQKPAABELAVDTGKABEPVSKSECTEAEAGPAKGAOAAEAATAEGALKAEKKEGGS 900
Db 330 PKPEAPTTKEPAPTTKEPAPTT-----APKPAPTTKEPAPTTTKEPAPTTTKEPAPTTTKE 379

901 GRATTAKSGAPQDSSTATCSADEVDEAGGDKNLLSPRPSLLTPTGDPNANASPKP 960
Db 380 -PSPTPKPEPAPTTTSAPTTKEP-----APTPTKSAPTTTKEPAPTTTKEPAPTTTKEPAP 418

961 LDLKQLKQRAAIPPTQVTKVHEP-----PRED-APTAPPPAPPPQNLQESDAPQ 1014
Db 419 -----SPTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTT 462

1015 PGSSPRGKSRPAPPADKEAFAEAQKLPQDPP-----CWTSGLPFPVPPPREVIKASPHAP 1070
Db 463 TKKPAFTAPEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAP 522

1071 DPSAFSAPGHPPLPLGLHDTAPVLPPTTINP--PPLISSAKHPSVLERQIGALSQGM 1129
Db 523 TPTT-----PEEPAPT--TPKAAAPNTPKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKE 563

1130 SVQLHVPYSEHAKAP-----VGPVTMGLPLPMDPKLAPSGVKQOLSPRQOAGPPESL 1184
Db 564 -----PTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAP 611

1185 G---VPTQAEASVLRGTALGVSFPGSITKGIPTSRVPSDAITYRGSITGTPADVLVKG 1241
Db 612 SDKPAFTTP-----KGTA-----PTT--PKEPAPT-----TPKEPAPTTPKG 646

1242 TITRIIGEDSPRLDGRDLSLPKHVIVGKKGHVLSEGGMSVTCSEKDRSSSGPP 1301
Db 647 TAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTT 689

1302 HETA--APKETYDMMEGRVGRALSSASIEGLMGRAIPP---ERHSPHLKKEQHHRGSIT 1356
Db 690 KETAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTT 740

1357 QGIPRSYVEAQEDYLRREAKLLKREGTP-----PPPPPSRDITAEYKQTQALGLPLKLPAP 1411

741 ESTPE-----LSAETPKALENSPKPEPGVPTTKT-----PAATKPE- 776
1412 EGLVATVKEAGRSIHIEPRELRHTE-LPLAPRPLKEGSIT-----1452
777 --MTTAKD-----KTERDLRTTETTTTAAAPKMKETATTTTEKTESKITATTQVTS 828
1453 ----QCTPLKYDTGAS-----TTGSKKHVRSLSIGSPORTPPVPHPLDVMADARALER 1501
829 TTTQDTTPFKITTLTKTLAPKVTITTKTITTTTINMKPEET-----AKPKDR 876
1502 ACVEESLKRPRGTASSSGS--TARGAPVIVPELGKPRQSLTYEDHGAPPAGHLPRGSPV 1560
877 ATNSKATTPKPKPTKAPKPKTSTTKPKTMPRVKPKTTP-----TPRKMTS 923
1561 TWRE--PTLRLQSGLSSSKASQDRKLTSTPREIAKSPHSTVPEHHPHPIPSVYELLRGV 1618
924 TWPENLPTSRIBAMLQT-----TTRPNQ---TPNSKLVE-----VNPKSEBAGGA 966
1619 SGVD---LYRSHIPLAFDPTSIPIRGIPLDAAAAYLPRHAPNPTYPHLYPPYLIRGYD 1675
967 EGETHMLLRPHV---FMPEVTP---DMD-----YLPR-----993
1676 TAALENROTIINDYTSQ-----QMHNHTATAMAQRA 1707
994 ---VPOGIIINPMLSDQYINIDVPSRTARAITRS 1026

RESULT 28
US-07-757-022B-42
Sequence 42, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserik, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170

Qy	1385	--PPPPSRDLTEAYKTQALGPLKLKAPEHGVATVKEAGRSIHETPREELRHTP-E-LPL 1444
Dd	797	ENSPKPEGVPVTTKT-----PAATKPE-----MTTHAKO-----KITERDLRTTPETTTA 840
Qy	1442	APRPLKEGSIT-----QGTFPKYDTGAS-----TTGSKKHD 1472
Dd	841	APKWTKETATTTEKTTESKITATTTQVTSITTQDTPFKITILTKTTTTLAPKVTTTKKTIIT 900
Qy	1473	VRLSIGSPGRTPPVHPVLDMADARALERACRYEELSLSRPGTASSSGS-IARGAPVIYP 1531
Dd	901	TTEIMNKPBET-----AKPKDRATNSKATTPKPQKPTKAPKPTSTKKPKTMP 948
Qy	1532	ELGKPRQSPLYEDHGCAFAGHLPRGSPVTMRB--PTPRLQEGLSSS---KASODRKLT 1586
Dd	949	RVRKPKTTP-----TPRKWTSTMPLENPISRIAEAMLOQTTRPNOTPHSKLV 995
Qy	1587	-----STPRBIAKSPHSVTPEHHPH-----PISPYEHLRLRGVGDLYRSHI 1628
Dd	996	EYNPKSEDAGABGETPHMLLR-PHYFMPEVTPDMYLPVFPNQGIIN-----1043
Qy	1629	PLAFDPTSIPRGIPLD 1644
Dd	1044	PMLSDETNICNGKXPVD 1059
 RESULT 29 US-09-854-856-36 ; Sequence 36, Application US/09854856 ; Patent No. 6541252 ; GENERAL INFORMATION: ; APPLICANT: Walke, D. Wade ; APPLICANT: Hilbun, Erin ; APPLICANT: Donoho, Gregory ; APPLICANT: Turner, C. Alexander Jr. ; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides ; TITLE OF INVENTION: Encoding the Same ; FILE REFERENCE: LEX-0178-USA ; CURRENT APPLICATION NUMBER: US/09/854,856 ; CURRENT FILING DATE: 2001-05-14 ; PRIOR APPLICATION NUMBER: US 60/206,015 ; PRIOR FILING DATE: 2000-05-19 ; NUMBER OF SEQ ID NOS: 64 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 36 ; LENGTH: 2185 ; TYPE: PRT ; ORGANISM: Homo sapiens ; FEATURE: ; NAME/KEY: VARIANT ; LOCATION: (1)...(2185) ; OTHER INFORMATION: Xaa = Any Amino Acid ; US-09-854-856-36		
 Query Match 3.1%; Score 408; DB 4; Length 2185; Best Local Similarity 19.6%; Pred. No. 7.9e-15; Matches 513; Conservative 291; Mismatches 943; Indels 872; Gaps 114;		
Qy	147	PVSEPPSPDHTDELELVPPRLSKEELLQMDRVDRITWVEQQLSKLKQQQLEREAAK 206
Dd	39	PLSLPQPISAAPVQSPAAPPHERETV-----TATATSOVAQQPPAAAAFGEQAIVA 89
Qy	207	PRRP-----EKVSPPEPIESKHRSLVQIIYDENRKAEEAHRILEGLGPOVELPLY 257
Dd	90	GPAISTVPSTSKDRPVSQPSL-----VGSKEEPPPA 121
Qy	258	NQPSDTRQYHENIKINOAMEKKLILYFKRRNHARKOWKQPCORYDOLMALEKKVERIE 317
Dd	122	RCSGS-----GGSAKEPQEERSQQDDI-BELETKAVGMS 155
Qy	318	NNPERRAKESKV-REYYEKOFPEIRKOR-----ELOERNMQSVRGCGSLMSAARSE 369
Dd	156	NDGRFLKFDIEIGRGSPFTVKYGLDTETTVEAWCELQDRK-----TKSERQRF 205

; APPLICANT: Walke, D. Wade		Db		635	-DOHQOQYQOQPSISVLSGTVDSGGSSVFTESRVSSQOTVSYGSOH-EQAHSTGTVP	692
; APPLICANT: Hilbun, Erin		Qy		768	KPPATLGADGPPPG--PPT--	787
; APPLICANT: Donoho, Gregory		Db		693	HIPSTVQAOQPHGVVPPSSVAGQSQOQOPSSSSLTGVSSSQPIHQPOQOQGIQQTAPPQ	752
; APPLICANT: Turner, C. Alexander Jr.		Qy		788	RTSRAPLEPT-PASEATGAPTPPPAPPSPSAPPVVPVKEEBEETAAAPVE--EBEQK	844
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides		Db		753	QTVQVSLQTSSTSEATTA-----QPVSQOQAPQVLPQVSAGKQLPVSQPVPTIQGEPQI	807
; FILE OF INVENTION: Encoding the Same		Qy		845	PPAAEE--LAVDTGKAEFPVKSECTEAEAGPAKGDAAEAATAECALKAEKKGSGR	902
; CURRENT APPLICATION NUMBER: US/09/854,856		Db		808	PVATQPSVVPVHSGAHFLV-----GQPL	831
; PRIOR FILING DATE: 2001-05-14		Qy		903	ATTAKSSGAPQDSSTATCSADEVDEAGDKNRLLSPRSLTLTGTCDPRANASPOKPLD	962
; NUMBER OF SEQ ID NOS: 64		Db		832	PTPL-----LPQYVPSQIPISTPHVSTAQTG-----FSSLPITWA-----AGITQPLL	874
; SOFTWARE: FastSeq for Windows Version 4.0		Qy		963	LKOLKORAAAIP-----PIQVTKVHEPPREDAAPTKAPPAPPPTPONTLOPESDAPQPG	1016
; SEQ ID NO 2		Db		875	TLASSATTAAIPGVSTWPSQLPTLLQPVTVQ-----LPSQVHPQLLP-----AVQSMG	923
; LENGTH: 2382		Qy		1017	SSPRGKSRPAPPADKEAFAAEAAQKLPDPWPCTWSGLPPVPVPPREVIKASPHAPDPSAFS	1076
; TYPE: PRT		Db		924	I-----PANI-GQAAEVPLSSGD--VLYQGFPPRLPPQY-----PGDSN	959
; ORGANISM: Homo sapiens		Qy		1077	YAPPGHPLGLHDTARPVL--PRPTTIGNPPPLISSAKHPSV--LEQIGAIQOQMSV	1131
; NAME/KEY: VARIANT		Db		960	IAPSSNVASVCIHST---VLXPMPTEVLATPGYFTVTVQVYESNLLVPMGGV--GGQV	1014
; LOCATION: (1)...(2382)		Qy		1132	QLHVPIYSEHAKAPGVPTMGLPLPMDPKLAPFSGYQEQLSPRGAGPPEISLGV-----	1186
; OTHER INFORMATION: Xaa = Any Amino Acid		Db		1015	QVSPGGSQAQAPTSSQAV-----LESTQGV-----SQVAPAEVAVAQQA	1058
US-09-854-856-2		Qy		1187	--PTAQEASVLGTALGVSPPGSIKGIPTSRVPSDAITYRGSITHGTPADVLYKGTIT	1244
Query Match		Db		1059	TOPTTLIASSV--DSAHSDVASG--MSDG--NENVPSSSG-----RHEGRTT	1098
Best Local Similarity 19.8%; Pred. No. 8.8e-15;		Qy		1245	RIIGEDPSRLDRGREDSLPKGHVIEGKKGHVLSYEGGMSVTQCSKE-----	1292
Matches 513; Conservative 291; Mismatches 943; Indels 872; Gaps 114;		Db		1099	KHYRKSIVRSRHEKTSRPLRLNLSNKGD-----RVVECOLETHNRKMVTFKPD	1150
147 PVSPPPPHTDPELELVPPPLSKEELIQNMDRVDREITWVEQQIISKLKKKQOQLEEEAAK		Qy		1293	-DGRSSGPPHETAAPKRTYDMMEGRVGRASISASIEGLMGRAPPERHSPHHLKQHHI	1351
99 PLSLPQSPAPVQSQAPPEHRETV-----TATATSOVAQPPAPAAAPGQAVA		Db		1151	LDGDN---PEEIIATIMVNDPI---LAIERESPDQVREII---EKADEMLSEDSVS	1198
207 PPBP-----EKVSPPPPIESKHSRLVQIIYDENRKAEEAARILEGLGQVQLPLPLY		Qy		1352	RGSIQIGIPRSVVEAQEDYLREAKLLKREGTTPPPPPRDLTEAYKTOALGPLKLPKH	1411
150 GPAPSTVPSSTKDRPVSQPSL-----VGSKEEPPPA		Db		1199	EPEGDQGL--ESLQGGDDYFGSGQKLEGEFKQPIPASSM-----PQIGIPT	1244
258 NQPSDTRQVHENTIKINQAMRKULLIFKRNHARKQWKQFCORYQOLMEALEKKYVERIE		Qy		1412	EGLVATVKEAGRS--IHEIPREELRHTPELAPRLKEGSIQGTPLKYDTCASTTGSK	1469
182 RSGSG-----GGSAAKEPQBERSQQDDI--EELETKAVGMS		Db		1245	SSLTQVHVSAGRRFVSPVPSRLRESKVPP-----SEIT-----DTVAASTAQS	1289
318 NNPERRAKESKV--REYVEKQFPEIRKQ-----ELQERMQRVQGRGSLMSAARSE		Qy		1470	-----KHDVRSI-----IGSPGRTFFPVPHPLDVNMADARALE	1500
216 NDRFLKFDIEIRGSEFKTVYKGLDTETTVAVWCBLQDK-----LTKSERQRF		Db		1290	PGMNLSSASSLSLQAFSELRAQWTEGTPAPPNFSTGPTFPVVP-----	1338
370 HEVSEIIDGLSEQENLEKQMRQLAVIPMLYDADQORIK-----FINNMGLM-ADPMKVYK		Qy		1501	RACYEBSLSRPGCTASSSGSITARGAP-----VIVPELGRKPRQSL--TYEDHCAPPA	1551
266 KEAEMLKGL-QHPNIVR-----FYDSWESTVKGKCVILVTELMTSGTLKTYL		Db		1339	---FLSSIIAGVPTTAAATAPVATSPNDISTSVQSEVTVPTVEEGIAGVATSTGVTS	1395
425 DR-----QVMNWSQOEKETPREKPMQHPK-----NFGLIA		Qy		1552	GHLPRGSPVTREPTPLQEGSLSSSKASQDRKLTSTPREIA---KSPHSTVPEHPHPI	1608
314 KRFPKVMKIVLRSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGTSVKIGDLGL--		Db		1396	GGI-----PIPVSESPLSVSVSS-----TIIPAVSISTTSPSLQVPTSTSEIV	1441
456 SFLERKTVAECLV-----YYLTQKNENY-----KSLVRSYRRRGKSQOQOQOQ		Qy		1609	SPYHLLRGVGDVLYRSHIPLAFDPTISPRGIPLDAAAAAYLPHRLAPNPTYPHYLPY	1668
372 ATLKRASFVSGTGTPEFVAPENYEBKYDESVDVYAFGCMLEWATSEYPYSECQNAQI		Db		1442	-----VSSTALYPS-----VTVSATSASAGSGSTATGPK-----PPA	1473
502 QOQOQOQOQO-----MPRSSQ-----EEKDEKEKEKEKEKEKEKEKEKEKEDE		Qy		1669	LI-----RGVPTDAALENRQ-----TIINDYITSQOQMH	1696
432 YRRVTSVGRPASDKVAIPVKEIIEGCRQNKDERYSIKOLLNHAFPOEETGVRVELAE		Db		1474	VVSQAAGSTTVGATLTSVSTTTTSPFSTASQLSIQLSSSTSTPTLAETVVSAAHSLDKTS	1533
548 EKTDDTSGEDNDEKAVASGRKTANSQGRKRGRITRSMANESE-EAITPOQSALAS		Qy				
492 E-----DDGEKIAIKLWLRIDIEIKLKGKYKDNEAIEFSDLRDVPEDVAQ---		Db				
607 MELNESSRWTEEBEMETAKGLLEHGRNWSAIARMVGSKTVSOCKNFYFNYKKQNLDLIL		Qy				
539 -EMVESGYCEGHDHKTMAKAIDR-----VSLIK-----RKKEQQLVR		Db				
667 QQHKLWEXERNARRKKKA-----PAAASEEAAFPVVEDEEMEASG		Qy				
577 EQQKKQKESSLKQVQESSASQTGIKQLPSASTGIPASTTSASVSTQVPEEPEA--		Db				
710 VSGNEEMVEEABALHASGNEVPRGCSGPATVN--NSSDTEIIPSPHTEAAKDTQNGP		Qy				

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QY 1697 HNTATAMA-----QADMLRGLSPR-----ESSLALNYAAGRGIID 1733
Db 1534 HSTTGLAFLSAPSSSSPGAGSVYSIQPGLHPLVPSVIASFPILPQAAGPTSTPL 1593
QY 1734 LQVPHLPVLVPTPTGTATMDRLAYLTAQPPSSSRHSSPLSPGGP-THLTPTTTS 1792
Db 1594 LQVPSIPPLVQVANPAV---QOTLIHSQOP-----ALLPNQPHTHCP----- 1636
QY 1793 SSERDRDRDRDREREKSLTSTTTVEHAPIWRPGTEQSSGSSGGGGSSSRPA 1852
Db 1637 -----EVDSDTPKAPGIDDIKTLEE-----KLSLFSHSSGA----- 1671
QY 1853 SHSHAHQSPISPTODALQORPSVLHNTCMKGI-ITAVEPSKPTVLRSTSTSSPVRPA 1911
Db 1672 -----QHASVLETS-----LVIESVTGPIPTAVAPSK--LLTSTT-----S 1708
QY 1912 TPTPTHCPGLGTLGVYPTLMEPVLLPKEARVARPERPRADTGHAFKAPPARSGLEP 1971
Db 1709 TCLPPTNLPLG-----TVALLPVTVPVTPGQVSTFVSTTTSGVKP 1747
QY 1972 ASSPSKSEPRPLVPPVSGHATITARTPAKNLAPHASPDPPAPPASADPHREKTS-KP 2030
Db 1748 GTAPSPPTKAPVLPGVTELPAGTLPSEQL-----PPPPGPEL-----TQSQOP 1792
QY 2031 FSIQELRLSLGVHSGSSYSGVEPVSPVSSPSLTHDKGLPKHLELDKSHLEGLRPQ 2090
Db 1793 LEDLDAQLR-----RTLSPXITVTSV-----1815
QY 2091 PGVPLKGGBAHLPHURPLPE---SQPSSPLLOTAGV---KHQRVVTTLAQHISEVI 2143
Db 1816 -GFSVMAAPTA-ITEAGTQPKGVSGVKEGCVLATSSGAGVFMGRFQVSVAA----- 1866
QY 2144 TDYTRHHQQLSAPLPAPLYSPGASCPLDLRRPDLPLPPP-----DHGAP 2193
Db 1867 --DGAQKEGNKSEDAKSVHFESSSTSSSVLSSSPSTLVKPEPNGITIPGISDVPS 1924
QY 2194 ARGSPHSEGGKSPENKTS-----VLGGGEDGIE-----PVSPPEGMTE 2233
Db 1925 AHKTASEAKSDTGQTKVGRFQVTTTANKVGRFVSVKTEDKITDPKKEGPVSPFMDL 1984
QY 2234 PGHRSRAVTVLYRDOEQTEPSRMGSKSPGNTSQP--PAFPSKLITESNANVSKSQEINK 2292
Db 1985 EQAVLPAVTPKKEKP-ELSEPSHLN---GPSDDPEAAFLSRDVEDDGGSGSPHQLSSK 2039
QY 2293 KLNTNHRNPEVYNISQPGTEIFNMPAITGTGLMTYRSQAVQ-----EHASTNMLEA 2344
Db 2040 SL-----PSQNLSSLSNSFNSTWSSDNESDIEDDLKLERLRLDKHLKEIQDLOS 2092
QY 2345 IIRKALMGKYDQWEEPSPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGGGKAK 2404
Db 2093 RQKHETESLYTKLGKYP-----AVIIPPAPLS---GRRRRTKS-----KGS 2133
QY 2405 VSGRPSRKAQP-APGLASGRPPPV-----SSVHSEGD 2438
Db 2134 KSSRSSSLGNKSPQLSGNLSGQSAASVLHPQOTLHPGN 2172
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RESULT 33

```
US-07-757-022B-14
; Sequence 14, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Geaner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
```

```
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cseri, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-14

Query Match 3.0%; Score 400.5; DB 4; Length 941;
Best Local Similarity 21.4%; Pred. No. 7.2e-15;
Matches 259; Conservative 116; Mismatches 484; Indels 351; Gaps 55;

QY 520 KDEKEKEAEKEEKEPEVNDKEDLLKEKTDGTDGDENDKEAEVASKGRKTANSQGRKK 579
Db 2 KDKK-KNRTKKXPTKPPVDEA-----GSLDNGDFKVTTPDTSTTOHNVKSTS 50
QY 580 GRITSMANEANSEAIIP-QQSABLASMELNESSRWTEEMETAKKGLLEHGRNWSATA 638
Db 51 PKIT--TAKPINRPSLPNSDTSKETSITVNKETTIVTKETTTTNNKQTSDDGKEKTTSA 108
QY 639 RMVGSKTYSQCKNFYFNVKRQNLDEILQOHKLME---KERNARRKKKAPAAASEEAA 695
Db 109 KETQSIKTSADL-----APTSKVLAKPTPKAETTKGPAITTPKEPTTTTPKEPAS 161
QY 696 FPPVVEDEMEASGVSGNEEMVEEAEALHASGNEVPREGCSGPATVNNSSDTEISPSH 755
Db 162 TTP-----KEPT-----PTTKSAPTTKPEAPT 185
QY 756 TEAAKDTGONGPKPATLGADGPPGPPPTPRRTSRAPTEPTPASEATCAPTP--PAP 813
Db 186 TTKSAPTTTPKEPAPTTT-----KEPAPTTKPEPAPTTTKEPAPTT--TKSAPTTTPKEPAPT 239
QY 814 SPSAPPVVVPEKEEETAAAPVEEGEBQKPPAAAEALAVDTGKAEEPVKSECTEAEBSG 873
Db 240 TPKKAPATTPKE--PAPTTPEPTTTTPKEPAPTTKEPAPTTKEPAPTT-----APKK 290
QY 874 PAKGKDAEAAATACALKAEKKEGSGRATTAKSSGAPQDSQSSATCSADEVDEAEGD 933
Db 291 PAPTTTPKEPAPTTTPKEPAPTTTKE-----PSPTTPKEPAPTTTTPKEPAPTTTKEP 338
QY 934 KNRLLSPRSLTTPGDPANASPOKPLDLKQLKQRAAIPPIQVTKVHEP-----PREDA 989
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Db 339 -----APTTKSAPTTPKEP-----SPTTKEPAPTTPKEPA 370
Qy 990 --APTAPAPPAPPPQNLQSPESDAPQPGSGSRKSPAPPADKEAFKAEAKLPGDPP 1047
Db 371 PTPPKKPAPTTPKEPAPTTPKEPAPTTPKPAAPKPAAPKPAAPKPAAPKPAAPK 430
Qy 1048 -----CWTSGLPFPVPREVIVKASPHAPDSAFYAPGHPGLGLHDTARVLPRLPTTIS 1103
Db 431 EKLAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPT 484
Qy 1104 NP-PPLISSAKHPSVLERQIGALSQMSVQLHVPVYSEHAKAP-----VGPVTMGLPLPMD 1157
Db 485 TPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPT 525
Qy 1158 PKGLAPFSGVQKQOLSPRGOAGPPELSG--VPTAQEASVLRGALSGVPGGSITKGPS 1214
Db 526 PKKPAP-----KELAPTTTKEPTSTSDKPAPTTP-----KQTA-----PT 561
Qy 1215 TRVPSDAITYRGSITHTGTPADVLVYKGTITRIIGEDSPSLDRGRDPSLPKHVYVEGKK 1274
Db 562 T--PKEPAPT-----TPKEPAPTTPKGTAPTTPKEPAPTTPKPAAPKPAAPK 605
Qy 1275 GHVLSYEGGMSVTQCSKEDGRSSSGPPHETA--APKRTYDMMGRVGRRAISSASIEGLMG 1332
Db 606 ---TTTKGPTSTT-----SDKPAPTTPKETAAPTTPKEPAPTTPKPAAPTPPT 651
Qy 1333 RAIPP---BRHSPHLKQCHHIRGSITQGIPIRSYVEAOEDYLREAKLKRQCTP----- 1384
Db 652 ---PPTTSEVSTPTTKEPTTIHKSPESTPE-----LSAEPPTKALEN 692
Qy 1385 PPPPPSRDUTEAYQALQGLKPKAHEGLVATVKEAGRSIHIEPRELRHTPE-LPLAP 1443
Db 693 SPKEPGVPTTKT-----PAATKPE---MTTAKD-----KTERDLRTTPTTTAAP 736
Qy 1444 RPLKEGSIT-----QCTPLKYDTGAS-----TTGSKKHVDR 1474
Db 737 KMTKETATTEKTESKIFATTTQVSTTTQDTPPKITTLTKTTLAPKVTITTKITTT 796
Qy 1475 SLIGSPGRFTFPVPHLDVMDARALRACVYESLSKSRPGTASSSGGS-IARGAPVIVPEL 1533
Db 797 EIMNKEET-----AKPKDRATNSKATTPKPKQKPKPKPKPKPKPKPKPKPKPV 844
Qy 1534 GKPRQSLTYEDHGAPFAGHLPGSVPTWRE--PTPRLOEGSLSSSKASQDRKLTSTPRE 1591
Db 845 RPKPTTP-----TPRKMTSTWPELNPTSRIAEAMLQ-----TTRPNQ 882
Qy 1592 IAKSPHSTVPEHHPHPLISPYEHLRLGVSGVD---LYRSHIPLAFDPTSIPRGIPLDAAA 1648
Db 883 ---TPNSKLVE-----VNPKSEDAGGAETPHMLLRPHV---FMPEVTP---DMD----- 924
Qy 1649 YVLPRLHAPN 1658
Db 925 -YLPR--VPN 931

RESULT 34

US-07-757-022B-84
; Sequence 84, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
PRIOR APPLICATION DATA:
CLASSIFICATION: 530
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 1022 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-84

Query Match 3.0%; Score 400.5; DB 4; Length 1022;
Best Local Similarity 21.4%; Pred. No. 8e-15;
Matches 259; Conservative 116; Mismatches 484; Indels 351; Gaps 55;
Qy 520 KDEKEKEAEKEEKEPEVENDKEDLLKEKTDGDDTSDEKDEKAVASKGRKTANSQGRRK 579
Db 83 KDKK-KNRTKKKPTPKPPVDEA-----GSLDNGDFKVTTPDSTTQHNKVSTS 131
Qy 580 GRITRSMANEANSEAITP-QQSAELASMELNESSRWTEEMETAKKGLLEHGRNWSALA 638
Db 132 PKIT--TAKPINRSLPNSDTSKETSIVNKETIVETKETTITNTKQSTDKKETS 189
Qy 639 RMVSKTVSQCNFYFNKYKQNLDBEILQOHLKME---KERNARKKKKAPAAASEEAA 695
Db 190 KETQSTIEKTSKADL-----APTSLVAKPTPKAETTTKGPALTTTPKEPTTTPKEPAS 242
Qy 696 FPPVVEDEMEASGVSGNEEVEAEALHASGNEVPRGECGSPATVNNSSDTSIPSPH 755
Db 243 TTP-----PTTIKSAPTTPKEPAPT 266
Qy 756 TEAAKDTGQNGPKPPATLGDGPPGPPPTTPRRTSRAPTEPTPASEATCAPTPP--PAPP 813
Db 267 TTKSAPTTPKEPAPITTT-----KEPAPITTPKEPAPITTPKEPAPT--TKSAPTTPKEPAPT 320
Qy 814 SPSAPPPVVPKEEKEETAAPVVEGEQKPPAAEELAVDTGKAEPEPVKSECTEABEG 873
Db 321 TPKKPAPTTPKE--PAPTTPKEPTTPTPKEPAPTTPKEPAPT-----APKK 371
Qy 874 PAKGKDAEAAEATAEGALKAEKKEGSGRAITAKSSGAPQSDSDSSATCSADEVDEAGGD 933
Db 372 PAPTTPKEPAPTTPKEPAPTTPKE-----PSPTTPKEPAPTTPKSAPTTPKEP----- 419
Qy 934 KNRLLSPRSLTPTGDPDRANASPOKPLDLKQLKQRAAAIPIQVTKVHEP-----PREDA 989
Db 420 -----APTTKSAPTTPKEP-----SPTTKEPAPTTPKEPA 451
Qy 990 --APTAPAPPAPPPQNLQSPESDAPQPGSGSRKSPAPPADKEAFKAEAKLPGDPP 1047

Db 871 -----PGATGPGAGRVGP-----PGPS-GNAGPP-----GPPGAGKEGKGPRGE- 912
QY 1690 ITSQOMHNTATAMAQRADML-----RGLSPRESSLALNYAAGPRGIDLSQVP 1738
Db 913 -----TGPRGPGVGPVGPAGXGSGPCGADGAPAGCTGPGQGIAGQGVV 961
QY 1739 HLPVLVPPT--PGTPATMDRLAYLPTAPOPFSSRHSSPLSPGGTHLTKPTTTSSSR 1796
Db 962 GLPGQGERGFGPLPGPSGE-----PKQGFSGASGERGPPGPMGPPGLAGPPGESGRE- 1015
QY 1797 ERDRERDRDREREKISLTSTTTTVEHAPITWRPCTEQSSGSSGSGGG-----GSSSRP 1851
Db 1016 -----GAFQAGSPGRDSDSPAKGDRGTGTAGPP 1045
QY 1852 ASHSHAHQHSPISPRTQDALQORPSVLHNTGMKGIITAVBPSKPTVLRTSTSTSPVRPAA 1911
Db 1046 GAFGAPGAPGVGP-----AGKSDRGCTGAPG-----AGPVGPAG 1082
QY 1912 TFPPTHCHLGGTLDGVYPTLMEPVLLPKAPRVARPERPRADTGH----- 1957
Db 1083 ARGP-----AGQGRGDKGETGEQDGRGIKGHRG 1112
QY 1958 -AFLAKPARSGLEPASSKSGSEPRPLVPVPSGHATIARTPAKNLAPHASDPDPAPPA 2016
Db 1113 FSLGQPPGPPGSGEGPGASGP-----AGPRGPPG 1145
QY 2017 SASDPHREKTQSPFSGIQLSLRSLGYSYSPGVEPVSPSPSLTHDKGLPKHLEE 2076
Db 1146 SAGAPKQGLNGLPGPI-----GPPGRGRTGDAGPVGPAGP----- 1184
QY 2077 LKSHLEGEPRKQPGVKLGGAHLPHLRPLPESQSPSSLLQTAPGVKHQ----- 2130
Db 1185 -----PPGPPGPPSAGPFGFSLP-----Qp-----PQKAHDGGRYR 1217
QY 2131 -----RVVTLAQHISEVITQDTRHHQQLSAPLPAPLYSFGASCPVL 2174
Db 1218 ADDANVVRDRDLVDVTTLSLSQOENIRSPESGRNPAR-----TC--R 1260
QY 2175 DLRRPPSDLYLPPPDHAPARGSPHSGGKRSPSPNKTSVLGG-----GEDGTEPV 2225
Db 1261 DLKXCHSDW-----KSGEYWDPNQGNLDALKVCNMETGETCVYPT 1303
QY 2226 SPPEGM-----TEPGHRSRAVPLLYRDEGEOTEPSRMGSKSPGNTSQPPAFPSKLTESN 2279
Db 1304 QPSVAQKNWYISKPKDKRHWFCESMTDGFQFEYG-----QGSDPADVAIQLT--- 1353
QY 2280 SAMVSKKQKQINKLNTNHNENEYNILOPG 2310
Db 1354 --FLRLMSTEASONITVHCNKNVAYMDQQTG 1382

RESULT 36

US-09-585-887-9

; Sequence 9, Application US/09585887

; Patent No. 6413742

; GENERAL INFORMATION:

; APPLICANT: Olsen, David R

; APPLICANT: Chang, Robert

; APPLICANT: McMullin, Hugh

; APPLICANT: Hitzeman, Ronald A.

; APPLICANT: Chisholm, George

; TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND

; TITLE OF INVENTION: FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT

; TITLE OF INVENTION: CELLS

; FILE REFERENCE: 225002030400

; CURRENT APPLICATION NUMBER: US/09/585,887

; CURRENT FILING DATE: 2000-05-31

; PRIOR APPLICATION NUMBER: 09/289,578

; PRIOR FILING DATE: 1999-04-09

; PRIOR APPLICATION NUMBER: 60/084,828

; PRIOR FILING DATE: 1998-05-08

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 9
; LENGTH: 1461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-585-887-9

Query Match 3.0%; Score 395; DB 4; Length 1461;

Best Local Similarity 21.4%; Pred. No. 2.6e-14;

Matches 378; Conservative 102; Mismatches 642; Indels 648; Gaps 82;

QY 722 EALHAGSNVPGECGSPATVNNSSDTEIPSPHTEAAKDTGQNGPKPPA-TLGAQDPP- 779
Db 77 ETKNCFGAEVPEGECPCVCDGSEPTD---QETTIGVEGDTGPRGRGAGPPGRDGIPI 133
QY 780 -----PGPTTPPRTSRAPIEPTPASEATGATPP-----PA 811
Db 134 QGLPGLPPGPP-----GPPGPGGLGNFAPQLSYGYDEKSTGGISVPG 176
QY 812 PPSPSAP-----PPVVPKEEKEEETAAAPVEGE-----EQKPPAAEELAVDTGKA 858
Db 177 PMGPSGRGLPGLPPGAPGPGQFQ---GPPGEGFEGCASGPMGPRGPPGPKNGKDDGEA 232
QY 859 EEPVKSECTEEAEHGAAGKDAEAEATAGALKAKEGGSGRATTAKSSGAPQSDSS 918
Db 233 GKPR-----PGRGPPGQAGRLPCTA--GLPGMKHGRGSLGDAKGDAGP----- 279
QY 919 ATCSADEVDEAEGGDKNRLSP-----RPSLLTPTGDPRANASPKQLDLKQLKQRAAIP 974
Db 280 -----AGPKGPGSPCENGAPGQMGPRGLPGERGRGAP-----GPAGARG 320
QY 975 PQVTKVHPREDAAAPTGA--PPAPPPQNLQPEDAPQOQSS--PRGKSRSPAP-- 1029
Db 321 NDGATGAAGPP---GPTGTPAGPPGPGGAVGAKGEA-GPGGPRGSGEGPQVRGEPGPPGP 375
QY 1030 -----ADKEAFAAEAKLPGDPPCWTSGLP--EPVPPREVIKASPHADPSAFSY 1077
Db 376 AGAAGPAGNPGADQPGKANGANGAP-----TAGAPFGARPGSPGPGGPGGPKGNS 430
QY 1078 APFGHPLPLGLHDTARVLPFRPTTISNPPPLISSAKHPSVLERIQIGAISQMSVOLHVPY 1137
Db 431 GEFGAGSGK--DTGAKGEPGPGVQVQGP-----GPAGEGKRG----- 467
QY 1138 SEHAKAPGVPTWMLPLPMDPKLAPFSGVKQBLSPRQAGPPESLGVPTAGEASVLRG 1197
Db 468 ---ARGEPGT--GLP-----GPPGERGGSGRGGFGADGVAGPKG 503
QY 1198 TA--LGSVPGSITKGP--STRVPSDAITYRGSITHTPADVLVYKGTITRIIGEDSPSR 1254
Db 504 PAGERGS--PGPAGPKSGPGEAGRPGEAGLPGAKGLT--GSPGSPGPDGK-----TGPPGPGAG 557
QY 1255 LD-----RGREDSL---PKGHVIEKGKGVLSYEGGM-----SVTQCSKEDG 1294
Db 558 QDGRPGPPGPGARGAGVWPGPGKGAAGEPGKAG-----ERGVPGPCGAVGAGPKDGE 612
QY 1295 RSSGGPHETAAPKRTYDMMEGRVGRRAISSASIEGLMGRAI PP--ERHSPHILKEQHHRG 1353
Db 613 AGAQGPP--GPAGPAGE---RGEQGPA--GSPGQGLPGPAGPGEAGKPGK----- 657
QY 1354 SITQGI PRSVVEAQEDYLRREAKLLKREGTTPPPPSRDLTEAYKQALGPLKXK--PAH 1411
Db 658 ---QGVGDLGAPGSPGARGERGFPGERGVQGGPPGA-----GPRGANGAPGN 702
QY 1412 EGLVATVKEAGRSIHEIPREELRHTPELPLAPRLKEGSIQTGTP---LKYDTGASTTG 1467
Db 703 DGNAG--DAG-----AFCAP-----GS--QCAPGLQGMPPGGAAGLP 736
QY 1468 SKKHD-----VRSLSGSPGR-----TFP--PVHPLDVMADARALERACRYEESLKRRPGT 1514
Db 737 GPKGRDGDAGPKGADGSGKDGVRGLTGTGTPGAPAGPD-----KGESGP 783
QY 1515 ASSSGGSIARGAPVIVPELGKPRQSPLYEDHCAPEAGHLPRGSPVMTREPTRLQEGSL 1574
Db 784 SGPAPTGARGAPGDRGEFGPP--GPAGFA--GPPGAD-----QOPAKGEPGDAGAKGD-- 834

1575 SSSKASQDRKLTSTPREIAKSPHSTVPEHHPHI-----SPYEHLLRGVGVLDYLRSHIPL 1630
835 -----AGPPGAPGAGPPGGIGNVAGPAGKAGSAGP----- 867
1631 AFDPTSPRGIPLDAAAAYLPHRLAPNTYPHLYPPYLRGYDPTAALENQTTINDYI 1690
868 -----PGATGPPGAGRVGP-----PGPS-GNAGPP-----GPPGAPGEGGKGRGE-- 909
1691 TSQMHNTATAMAQADML-----RGLSPRESSLALNYAAGPRGIIDLSQVPH 1739
910 -----TGAPGRPEVGGPPGPPGAGEKSGPCADGAPGAPGPPGQGIAGQGVVG 959
1740 LPVLVPPT--PGTATAMDLAYLTAPOPFSSRHSSSPSLSPGPFHLTKPTTTSSERE 1797
960 LPQRCGERGFPGLPGPSGE-----PKQGPASGASGERGPPGPMGPPGLAGPPGESGRE-- 1012
1798 RDRDRDRDREREKILSTTTVEHAP1WRPGTEOSSSSSSSSGGG-----GSSRPA 1852
1013 -----GAPGAGSGPRDGSPPGAKGDRGETGAPGPPG 1043
1853 SHSHAHQHSPIPTQDALQORPSVLHNTGMKGIITAVEPSKPTVLRSTSTSPVRPAAT 1912
1044 APCAPVAPGVGP-----AKSGDRGETGAPG-----AGPVGPVGA 1080
1913 FPPATHCPLGGTLDGVYPTIMEPVLLPKAPRVARPERPRADTGH----- 1957
1081 RGP-----AGPQGRGDKGETGEQDGRGKIGHRGF 1110
1958 AFLAKPAPASGLEPASSPSKSGSEPRLPVPPVSGHATIAITPAKNLAPHASDDPPAPPAS 2017
1111 SGLQGPFPGPSGEGQCPGASGP-----AGPRGPPGS 1143
2018 ASDPHREKTKSPFSQLELRLSLGVHSSYSPEGVPEVPSVSSPSLTHDKGLPKHLEL 2077
1144 AGAPGKDGKLNGLPGPI-----GPPGRGRTGDAGVPGPPG----- 1181
2078 DKSHLEGLERPKQPGVKLGGAHLPHLRPLPESQPSFSSSPLLQTAGVKHQ----- 2130
1182 -----PPGPPGPSAGDFPSFLP-----QP-----PQEKADHGGRYYRA 1215
2131 -----RVVTLAHISVITQDTRHHHPQOLSAPLAPLYSFPGASCPULD 2175
1216 DDANVVRDRDLEVDTTLSQOQIENIRSPESGRKNPAR-----TC--RD 1258
2176 LRPPSDLYLPPDHGAPARGSHSGGKRSPEPNTSVLGG-----GEDGIEPVS 2226
1259 LKCHSDW-----KSGEYWDPNQGCMLDAIKVFCNMETGETCVYPTQ 1301
2227 PPEGM-----TEPGHRSADVPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTENS 2280
1302 PSVAQKNWYISKNPDKRHWFCESMTDGFQFEYG-----GQSDPADVAIQLT---- 1350
2281 AMVSKKQKQINKLNTNHNREPNYNSQPG 2310
1351 -FIRLMSTEQNITYHCKNSVAYMDQQTG 1379

RESULT 37
US-09-289-578-9
; Sequence 9, Application US/09289578
; Patent No. 6428978
; GENERAL INFORMATION:
; APPLICANT: Olsen, David R
; APPLICANT: Chang, Robert
; APPLICANT: McMullin, Hugh
; APPLICANT: Hitzeman, Ronald A.
; TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
; FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
; CELLS
; FILE REFERENCE: 225002030400
; CURRENT APPLICATION NUMBER: US/09/289,578

; CURRENT FILING DATE: 1999-04-10
; PRIOR APPLICATION NUMBER: 60/084,828
; FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-289-578-9

Query Match 3.0%; Score 395; DB 4; Length 1461;
Best Local Similarity 21.4%; Pred. No. 2.6e-14;
Matches 378; Conservative 102; Mismatches 642; Indels 648; Gaps 82;
QY 722 EALHASGNEVREGCSGPATVNNSSDTSIPSPHTAAKDTGONGPKPPA-TLGDAGDP- 779
Db 77 ETKNCFGAEBPGECCPVCPPGSESPTD---QETTVGEDTGPGRGPAGPPGRDGP 133
QY 780 ----FGPTTPPRTSRAPIEPTPASEATGATPP-----GPPGPPGLGNFAPQLSVGYDEKSTGIGSV 811
Db 134 QFGLFPPGPP-----GPPGPPGLGNFAPQLSVGYDEKSTGIGSV 176
QY 812 PPSAP-----PPVVPKEEKEETAAAPPVEEG-----EOKPPAAEELAVDTGKA 858
Db 177 PMGPSGPRGLPGPPGAPGPPGQFQ---GPPGEPGFGASGPMGPRGPPGPPGKNGDDGEA 232
QY 859 EEPVSKSETEAEEGPAKDAEAAEATAEGALKAEKKEGSGRATTAKSSGAPQSDSS 918
Db 233 GKPR-----PGERPPPOGARGLPCTA--GLPMKGRHGFSGLDGAKGDAGP----- 279
QY 919 ATCSADEVDEAGGDKNLLSP---RPSLLTPTGDPANASPPKPLDLKQLKQRAAIP 974
Db 280 -----AGPKGPGSGENGAFQMGPRGLPGERGRGAP-----GPAGARG 320
QY 975 PIQVTKVHEPPREDAAPTKA-PPAPPPQNIQESDAPQPPGSS--PRGKRSRAPP-- 1029
Db 321 NDGATCAAGPP---GPTGAPGPPGPAVAKGEA-GPQGRGSEGGVGRGEPGPP 375
QY 1030 -----ADKEAFAAEAQKLPDPPCWTSGLP-FPVPPREVIKASPHAPDPSAFSY 1077
Db 376 AGAAGPAGNPGADGQGAKANGAAG-----IAGAPGPGARGSPGPGGPPGPKGNS 430
QY 1078 APPGHPLPLGLHDTARVLPRLPTTINPPPLISSAKHPSVLERQIGAISQGMVOLHVPY 1137
Db 431 GEPGAPGSKG-DTCAKGEPPGVGQGP-----GPAGEGKRG----- 467
QY 1138 SEHAKAPVGVTMGLPLPMDPKLAPFSGVKQEQLSPRQAGPPESLGVPTAQEASVLRG 1197
Db 468 ---ARGEPGPT--GLP-----GPPGERGGSGRGGFPFGADGVAGPKG 503
QY 1198 TA--LGSPGGSITKGP-STRVPSDSAITYRGSITHGTDPADVLYKGTITRIIGEDSPSR 1254
Db 504 PAGERGS-PGPAGPKGSGEAGRPOEAGLPKAKGLT-GSPSGPGDGK---TGPPGAP 557
QY 1255 LD-----RGEDSL---PKGHVIVEGKRGHVLVSEYEGM-----SVTQCKEDG 1294
Db 558 QDGRPPGPPGARGQAGVMGPPGKAAGEPGKAG-----ERGVPGPPGAVGAPGKGE 612
QY 1295 RSSSGPPHETAAPKRTYDMMEGRVCRATSSAIEGLMGRATPP-PRHSPHLKEQHHRG 1353
Db 613 AGAOGPP-GPAGPAGE---RGEQGA-GSPGQGLPGPAGPPGAGPGE----- 657
QY 1354 SITQIGIPRSYEAQEDYLRREAKLLKREGTPPPPPSRDLTEAYKTQALGPLK--PAH 1411
Db 658 ---QVPGDLGAPGSGARGERGPPGERGVQVQPPGA-----GPRGANGAPGN 702
QY 1412 EGLVATVKEAGRSIHEIPRELRHTPELAPRLKEGSIQTGP-----LKYDTGASTTG 1467
Db 703 DGAKG---DAG-----APGAP-----GS--QGAPGLQMPGCAAGLP 736
QY 1468 SKKHD-----VRSLLGSGR-----TFP--PVHPLDVMADALERACYEESLSRPGT 1514


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Db      848  TGAQPAQHHPADPLGLPRADRLQRLVLRQPP---ERAGTPSAGQHPAHOAGTDPG  904
QY      1385  -----PPPP-----PSRDLTAYKTQALG-----PLKLPAHEGLVATVKEAGR  1423
Db      905  ERPVPEPEQARGASRRPLRPTLAPTLRGAAVGGRGHLQPOQAGR-HRGAPGTARRAGR  963
QY      1424  SIHEIPEP-----EELRHTPELPAPRPLKEGSIQ-----1453
Db      964  ---DVPRLRGARARRRRGHGRVVEERGERAGRRDRLLHLRPPORPOLPAQLRARA  1020
QY      1454  -----GTLKYDYGASTTGSKKHDVR-----SLIGSPGR---TPPPVHPLDVMD  1495
Db      1021  DRRRAPPGGDDPRAAGGDDHLDARRHLRHARHPALAEQPARLPARGIRPRTVRR  1080
QY      1496  ARALERACYEESLKSPGTASSGGSIARCAPVIVP-----ELGKRQSPILT-----1542
Db      1081  VR-----RYRP-TARAPAHPRPQRPAPALPATRRLQRDRRRVHPLAGLVRTRR  1128
QY      1543  -----YEDHGAPFAGHLPRGSPVVTWREPTP-----RLQEGSLSSSKASQDKLSTPR  1590
Db      1129  RRRRLRPLRHREP---GHRPLRHRHRMRPLPPAAGTRPRPGNLATLGAAG-----1178
QY      1591  ETIAKSPHSTVPEHHHPHPISPYEHLRGVSGVDLYRSHIPLAFDPTSIPIRGIPLDAAAYY  1650
Db      1179  -----DPAP-----PPGFLPLVPRRRQRTRTAA--1202
QY      1651  LPRH-----LAPNYPYH-----LYPPVYLIRGYPDTALENRQTIINDYITSQMHNT  1699
Db      1203  -RRHREGPGAQNGPSHGSGGLPMGPKVVRIVTREETAIATCERDLQDKALARWENQ  1261
QY      1700  ATAMAQADMLRGLS-PRESSIALNVAAGRGII-----DLSQVP-----H  1739
Db      1262  ASRLAQLSDAERAAAHARASL---HALARTGLAGRAITGEDRKIPOARPRTRERARH  1318
QY      1740  LPVLVPP-----TPGTATAMDRLAYILPTAPQPPSSHRSSPSLPGPQTHLTKPTTSSSE  1795
Db      1319  -----PPGRGITATPPPPKQRPAPGPRRQARCRQGSPPANPAGARRRRPPRRGSPA  1373
QY      1796  RER-DREDRDREREKS-ILNTSTTIVEHAPITWRPGTEQSSSGSSGGSGGSSSRPAS  1853
Db      1374  RPRFCPRQRPRGTQQRSPARTPRPAPEDRRNNAHFGTVARPPATGRP-----ARTAPGA  1428
QY      1854  HSHAQHSPISTQDALQORPSVLHNTGMKGIITAVEPSKPTVLSTSTSTSPVPAATF  1913
Db      1429  HRPAHRTATAARR---GQPSVPRATGTRRSRTAPGAPQPAARQPGPRPRGPRT--1482
QY      1914  PPATCPGLGTLGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLPAS  1973
Db      1483  PAATPAP--GT-----PARPRQSRPRRRRTRTA-----PARRRL-PAR  1520
QY      1974  SPKSGSEPRPLVPVSGHATIAITPAKNLAPHASPDPPAPPASADPHREKTQSKPFSI  2033
Db      1521  QRSAAITR-----RTHRAMQRHPHR---PPATGRPRPPPGAPGPRQPR-----1561
QY      2034  QELELSLGYHSGSYSPGVEPVSPVSSPSLTHDKGLPKHLELDKSHLEGELRPKQGP  2093
Db      1562  -----LRSPRHG-----HRLGADROGRP--1580
QY      2094  VKLGGEAHLPHLRPLPESQPSPLLOTAPGVKGHORVVTLAQHISEVITQDTRHHQ  2153
Db      1581  ---AQTRH-PLRLPGSRRO-----GRQRPATA-----RRRQ  1609
QY      2154  QLSAPLPAPLSPFGASCPLDLRRPPSDLYLPPDHGAPARGSPHSEGGKRSPEPNKTS  2213
Db      1610  RQROPAPRPHRP-----LVRRVPT-----PP---GPAP-----RPRERTQRTA-1648
QY      2214  VLGGEDGIE 2223
Db      1649  --GGGRSGVE 1656
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US-09-252-991A-17231
; Sequence 17231, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17231
; LENGTH: 2294
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17231
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Query Match 2.9%; Score 382.5; DB 4; Length 2294;
Best Local Similarity 21.1%; Pred. No. 2.4e-13;
Matches 463; Conservative 177; Mismatches 876; Indels 679; Gaps 105;

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QY      735  ECGS-PATVNNSSDTSIPSPHTEAAKDTGQNGPKPPATLGADGPPPGPPTPP-----RR  788
Db      83   ECRGKPARWHR-----LPRPAEA-----GRPHRGCGRGPRRRPLRQPGAGSARR  129
QY      789  TSRAPIEPTPASEATGATPPPAPSPSAPPVVPVKEEKEETAAPPVVEEGEEQKPPAA  848
Db      130  QCRLR-EPRP-----GGFGQGVPPADRARRP-----RRIRGRGRAGP--167
QY      849  BELAVDTGKAEBPVKSECTEEAEAGPAKGDAAEA-----TABGALKAEEKGSGSRA  903
Db      168  -----REARGPGEFGRGIPAGARHCRAAAGVL-----RQGAAGPA  205
QY      904  TTAKSSGAPQSDSSATCSADEVBAEGDKNR-LLSPRPSLLTPTGD-----PR  952
Db      206  PPARSS--PR-----RAGGGIQRGRLGNRLPAAATGQPRRPHWSPVR  249
QY      953  ANASP-----QKPLDLKQLKQRAAAITPQTVKHPPEPREDAAPTKPAAPP  1001
Db      250  APAAPAGAVPTGGPCRRVLYLHRQPAASRGVGVQ-----PRRPGQLRPGDARPA  302
QY      1002  -----PQNLQPEDAPQOPGSSPRGKSRSPAP--PADKE  1033
Db      303  GAGDGRRCQDRHPRRREGLRREARDAQRPQDRQRLRPGGARRRPREPARALPAAG  362
QY      1034  AFAAEAQKLPGDP-----PCWTSG-----LP-----PFVPPRE-VIKAS-----P  1067
Db      363  GRLGGAHPRPGQFATAGYRPAADAGGAADPLRRLHLFRTGPRQRALEADALRLRLP  422
QY      1068  H-APDPSA-----FSYAPPGH-----PLPLGLHDTARPVLPRPTISN  1104
Db      423  HRRPVRAEPGLLGHRSISNDASHRRSLRHPGRRQRKPARRPHDHAASRRPDTGRR  482
QY      1105  PPPLIS-----SAKHPSVLBRQICAIISQMSGVQLHVPYSEHAKAPVG--VTMG  1151
Db      483  PRRRSLHAAADGQPCAAERPRRRPQPCAGARRPTAGDAHPAQHHRPSGAGQPARATAR  542
QY      1152  LPLPM-----DPKKLAPFSGVKQQLSPRGOAGP---PESLG  1185
Db      543  LPAPVRGECTGPRRGAGRS DAGALRALHRRPRRSGAQAHVGOHQ--RLGOAEADHPAQRG  600
QY      1186  VPTAQEASVLRGTALGVSVP-----GGSITKGIPTSTRVP-----SDSAITYRGS  1229
Db      601  LGRREGLPVARTLPAEPAPAPAGAAVPHQPRLRPLPGHARRPQPTGGARAHRG--658
QY      1230  THGTTPADVLYKGTITRIIGEDSPSRDLRGREDSLPKGVH-IYEGKKGHVLSVEGGMSTQ  1288
Db      659  --GDPQH-----PRVRARTVAALARPQDARPPFAIPAAVGYRHRPGLAAGLAVRP  709
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Qy	1289	CSKEDGRSSG-----PPHETAAPKRTYDMMGRVGRVAISSASIEGLMG	1333
Db	710	ADAEGRRRRAQVAHPHRRDPGAGHRPPGCGAAAGDRA--ATPGALPRRRHQPAGCGGG	767
Qy	1333	RAIP-----PERUSPHILKEQ-----HHIRGSITQIGIPRSVVAEQEDYLREAK	1376
Db	768	RRRPLGDDHRRRAVRQORQORARRVPAAAAHRRRPAQCQG--PGAGHRAIATTGRSPRC	826
Qy	1377	LKREGTTPPPPSRDLTEAYK--TOALGFLK-----LKPAH-----	1411
Db	827	ATRPTGNCPRAPRRSPSTSSARPPATPAASPCKGAATPSRWRPMPAKAAHATAGWKSPY	886
Qy	1412	-----EGLVATVKEAGRSIHETPREELRHTPELPLAPRLPKGSGTQGTPLKYDTGAST	1465
Db	887	SRARNERLPQLLRGAGARPARPEFDH-----LVPRP-----AAAPGQLRTVGLGDQP	937
Qy	1466	TGSKKHVDVSLIGSP--GRTFPPVHPLDVMADARALERACYEESLSKR-----	1511
Db	938	LGAADPAVPGDLRLPRAHRAGPAQGEHGAESRRQORAGRRORHRRRRAGDDQATHGRG	997
Qy	1512	PGTASSGGSIARGAPVIVPELKGKPROSPITYEDHGA--PFAGHLR-----RGSPVTMR	1563
Db	998	PGPAQAQAGCRAAQOPVRVALVRDHPARFQGDHRADELRLPGLPARRTDRGREGDPRGR	1057
Qy	1564	EPTPRL-----OEGSLSSK-----ASQDR-----KLSTPREIAKSHSTVPE-----	1606
Db	1058	HAQURLVVRHRSAAAGHRRPLVHPGQPRPGCGQLAGLPRP--AQDPAQAPPHRWRVHRHQ	1116
Qy	1607	PISPYEHLRGVSGVDLYRSHIPLADPTSI PRGILPDLAAAYVLP-----	1652
Db	1117	FFPAGQRR-----RARRPCGDPFRTHPGAVP--AARGALPDLRDADQVRPGAGL	1165
Qy	1653	----RHLPANPTYPHLYPPY-----LIRGYPDTAALENRQTIINDVITSSOOMHNTATAM	1703
Db	1166	HGVLROPEPGTRAGLDGDLRPRRQERGPAGV--RQIRPARTASHRAPCGTTPAAG	1222
Qy	1704	AQRADMLRGLSPRESSIALNYAAGPRGIDLSQVPHLPVLVPTPGTPTATAMDRLAYLPT	1763
Db	1223	ARPGAARPGI--RLPAAIRPARMPR-----RVPQRRVQAQLRGTPAVAR-----	1268
Qy	1764	APQFFSRHSSPLS--PGGTHLTKPITTTSSRERDRDRDRDREREKSILTTTVE	1822
Db	1269	LHORNPGQSDRPPDRQHGAVDEBPPAPGAADNRQAQ-----LLHRAAVP	1314
Qy	1823	HAPI--WRPTEQSSG-----SSGSGGGGGSS-----SRPAS	1853
Db	1315	RSGVRTFPGHQPEGRAPPQVADHRAERHARGAGGCGDMDRQLPROPELHRRGPAR	1374
Qy	1854	HSHAHQHSITSP-----RTQALQORPVLNHTGMKGIITAVEBKPFTVLKSTSTSSP	1906
Db	1375	RPAGARHVAEPCPARPGRTATQAQGAESRRRAELGRRLRAV--PGR--HARRGVQRQLP	1432
Qy	1907	VRPANTFPATHCPLGTLDGVPTLMEPVLLPKEAPR---VARPERPRADTGHAFAPK	1963
Db	1433	QAADRGVVRPAGDPHRTGV-----ALRRQORFPLRGEGPLDARQPGPLRRLRHQGLDQP	1487
Qy	1964	PARGLEPASSPKSGSEPRPLVPVPSGHATITARTPAKNLAPHASDDP---PAPPASASD	2020
Db	1488	--RLGTQPARPLAGTAPGARAP-----RRVARTTAAGVAP--GPGGEGPAPPVAATA	1538
Qy	2021	-----PHREKTQSPFISQIELELSLGVHG-----SSVSPGVEVP	2055
Db	1539	GGAAGLRPGQAAEAAQGRARLPHQRRRRPR-----RAAGVRAQERQAAHRP-----	1584
Qy	2056	VSPVSSSLTH-----DKGLPKHLEELDKSHLEGEL-----RPKQCPVKLGEAA	2101
Db	1585	-----AQRLHLRLSRGVPHRQPQGRHRRGTVGARAPERCRRRRQPGPRSPFLVP	1639
Qy	2102	HLPHLRPLPESQSSSPLLOTAPGVK--GHORVVTLA-----OH	2138
Db	1640	GLPAAVGRPARPVRSADHCHQPGRRRAHSLRTDLAVPQAARGGGPPRPAESGRPAGRR	1699
Qy	2139	ISEVITODYTRHHFQQLASFLPAPLYSFPGASCFLVLRPPSDLYLPPPDHGAPARGSP	2198

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Db      1700 ASE-----EGRRRHGGQAAP---RLAGRPGGA-----RRPRT-----AAAGRQP 1739
Qy      2199 HSEGGKSPFNKTSVLGGGEGDIEPVSPPEGMTEFGHSHSAVYPLLYRDGEQTEFSRMG 2258
Db      1740 DQRLRRTQPGQQ---GRGQRTGADRQFAG---GHERA-----LRTGQR--HGSRQ 1784
Qy      2259 SKSPGNTSQPPAFSKLTE-----SNSAMVSKKQELNKLNTHRNEPEYNISOPG 2310
Db      1785 RRLAARRRQFEGRRRLARCPQRRAPAGFGTGEERGQLHQHQHGDGQRAQP-----AORG 1840
Qy      2311 TEI---FNMPAITGTGLMTYRSQAOEHASTNMGLEAIRKALMGKYDOWEESPPLSANA 2367
Db      1841 LDQERGQLPAVGRALPDRRQLARRHPCR-----LRPLRCRWGQGQLPPVPATL 1893
Qy      2368 FNPLNASASLPAA-----MPITAADGRSDHTLTSPGGGKAKVSG----- 2407
Db      1894 RRHLRQLHALAARRGAERHQSRRAAHLPARGSDPRRLPLRRHAAGGALRTQAGDHGRG 1953
Qy      2408 -RBSRRKAKSPACLASGDRPPSPVSSHSGDCNRRRTPLTNRVWEDRPPSSAGSTPF---P 2463
Db      1954 DQVHPRPRPADLRPRPQPGGDV-ADRQRRGP-----PDODAAAQORPPRPDP 2006
Qy      2464 YNPLMERLQAGVMASPPPPGLPAGSG--PLAGPHH 2496
Db      2007 GRPL-----GLV-----PPARPVGGRQLAGPLH 2031

RESULT 40
US-08-061-376-5
; Sequence 5, Application US/08061376
; Patent No. 6175000
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Djabali, Malek
; APPLICANT: Selleri, Licia
; APPLICANT: Parry, Pauline
; TITLE OF INVENTION: CHARACTERIZATION OF A CHROMOSOME 11Q23
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/061,376
; FILING DATE: 13-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen B.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9387
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)546-4737
; TELEFAX: (619)546-9392
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3969 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-061-376-5

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Query Match 2.9%; Score 380; DB 3; Length 3969;

Best Local Similarity 17.8%; Pred. No. 6.7e-13;
Matches 589; Conservative 357; Mismatches 1073; Indels 1270; Gaps 146;

QY	51	SHLSPGIIIOQRRRPSLLS-EPQGNERSQEUHLRPESHSYLP-----ELGKSMEMFIES	105
Db	679	SPLHSGTRFDMHKRSPLLRAPRFTP-----SEASHRIFESVTLPSNRTSAGTSSSGVSNR	733
QY	106	KRRRLLELPPDLRPPSLLATGQPGAGSEDLTKORSLTGKLEPYSPPPHTDPPELVLVPP	165
Db	734	KRRKRVSP---INSEP-----RSPSHMRTRSGRLSSSELSPLTPSPSVSSSUSISVSP-	785
QY	166	RLSKEELIQNMDRVDRITWVEOQISKLKKKQOOLEEBAKPPPEKVPSPPTIESKHS	225
Db	786	-LATSALNPFTTPSHSLT-----QSGSAEKQRPRIQTSAPEFSSSSPTPL-----	834
QY	226	LVQIYIDENRKAABAAHRIEGLGPQVELFLYNQPSDTQVHENIKINOAMRKKLILYFK	285
Db	835	-----FWFTPGSQTERGNKDKAPEELSKD-----	860
QY	286	RRNHARKQWKQPCORYDQDLMEALEKKVERIENPPRRAKESKVREYVEYEQFPEIRKORE	345
Db	861	-RDADKSVEXDK-----SBERDREKENKRESKEKR-----KKGSEIOSSA	903
QY	346	L-----QERWQSRVGORGSGLSMAAR-SEHEVSEIIDG-----LS	380
Db	904	LYPGRVSKKVGVEDVATSSAKATGRKKSSHSDGTILTSVLTGDTAVTKILIKK	963
QY	381	EQENLEKOMQLAVIPMLYDADOORIKFINMGLMADPMKVYKDRQVMNWSQEKETFP	440
Db	964	GRGNLEKTLNLDLGPATPSL-----EKEKTLCLSTPSSSTVK-HSTSIGSLMAQADKLPM	1017
QY	441	REXFMQHPKFGLTASTLERKTVAEVLVYYLTKKENYKLSLVSRRRCKSQOQQOQQ	500
Db	1018	TDK-----RVASLLKKAKAQLC-----KIEKSKSL-----	1042
QY	501	QOQOQOQOQPMRPSOEEKDEKEK-----EKEAEKEEKEPEVE--	539
Db	1043	-----KOTDOPKAQOESDSSETSVRGPRIKHVCRAAVALGRKCAVPFDDMTLSAL	1095
QY	540	--NDKEDLLKEKTDGTTSGDENDEKAVASGRKRTANSQGRRKGRITRSMANEANSEAI-	596
Db	1096	PWBEREKIL-----SSMGNDKSSIIA--GSEDAEFLAPPIKIPKPTRNKAPQEPVPK	1146
QY	597	--TPQSAELASMELNESSRWTEEMETAKGILLEHGRNWSATARMVGSKTVSOCKNFX	653
Db	1147	KGRSRRCGQCPGQVPCDGCVTNCJDXKPKFG-----GRN-----IKQOC----	1187
QY	654	FNYKKRQNLDEILQOHLKWKERNARRKKKAPAAAEEAAFPVPVVEDEBEMEASVSGN	713
Db	1188	CKMRKQNLQ--WMPSKAYLQOKAKAVKKEKSKTS-----EKDSESSVVVK	1235
QY	714	EEMVBEAEALHASGNVPRGECSG-----PATVNNSDTEISPSH-----TEAAKD	761
Db	1236	---VVDSSQKPTSAARDPAKPKSSSSPPPRKPVEEKSEGNVSAPGESQKATTPASRK	1292
QY	762	TGQNGKPPATLGADGPPGPPT--PBRRTSRAPTEPTASEATGATPPAPSPS---	816
Db	1293	SSQKVSQFALVI-----PPOPTTGPBRK--EVP-KTTPSEPKKKQPPPPESGPEQSKQK	1344
QY	817	--APPVPVVKEEBEETAAAAAPPVEEGE-----EQKPPA-----	847
Db	1345	KVAPRPSIPVKQPKPEKEKPPVNVKNQENAGTNLITLSLNGNSSKKQIPADGVHRIRVDF	1404
QY	848	-----ABE-----LAVDTGKAE-----EPVKSECTEBAEE	872
Db	1405	KEDCEAENWEMGGLGILTSVPIPTFRVVCFLCASSGHVEFYQCVCCEPFHKFLEC-NE	1463
QY	873	GPAK-----GKDAEAAEATAE-----	897
Db	1464	RPLEDQLENCCRCKFCHVCGRQHQATKQLECNKCNYSYHPCLGPNYPTKTKKKKV	1523
QY	898	-----GGSGRAITXKSGAPQDSDSSA-----TCSADEVDEAE	930

1524	Db	WICTKVRCKSGOSTTTPGKWDQWSDHPSLCHDCAKLFAGNFCBCLDKCYCDDDDYESK	1581
931	Qy	-----GDKNRLLSRPSLLTPT-----GDPRANASFPQKPLDL	963
1584	Db	MMOQCKDRWVHSCENLSDMEYELLNLPESVAYTCVNCTERHPAEMRLALEKELQISL	1643
964	Qy	-----LKQRAAIIPIQVTKVHEPPREDAAPTKPAAPPAPPPPPONTQOPES	1009
1644	Db	KQVLTALLNSRTTSHLLRYQAAKPPDL-----NPETESIPSRSSPEGDPDPVLTEVSK	1698
1010	Qy	DAPQOQSSPRGSKSRSPAPPADKEAFAAEACKLPGBPWCWTSGLPVPVPREVIKASPHA	1069
1699	Db	QDDQP-----LDLGEVGRKMDQGNVTSVLEFSDDTVKLIQAAINS	1739
1070	Qy	PDFSAFSYAPPGHPLPLGLHDTARP-----VLP-----RPPTISNPPPLISS	1111
1740	Db	DG-----GQPETIKKANSWKVSFFIORMERVFFWFSVKYSRFEWPNKVSNSGMLPN	1790
1112	Qy	AKHPSVL-----BROIGA-ISQMSVQLHVPHYSEHAKAPVPTMTGLPLPMDPKKLA	1162
1791	Db	AVLPSPSLDHNYAQWQREENSHTEQPPLMKKIIP-----APKPKGPEBDSPTPLHPPTTP	1846
1163	Qy	PFSGVQEQLSPRQAGPPESL-----GVPTAQEA-----	1192
1847	Db	ILSTDRSREDSP--ELNPPGIEDNRQCALCTLYGDDSDANDAGRLLYIGONETHVNCAL	1904
1193	Qy	-----SVLRGTALG-----SVPGGSITKGIPSTRVPSPSAITYRGSIT	1230
1905	Db	WSAEVFEDDDGSLKNVHMAVIRKQRCBFCQPGATV--GCCLTSCTSN-----	1952
1231	Qy	HGTPADVLYKGTITR-----IIGBDSRSLDRGREDSLPKGHVI-----YEG	1272
1953	Db	-----YHFMCRAKNCVFLDDKKVYQQRHD--LIGKEVVYPENGFEVRRFVDFDEG	2002
1273	Qy	-----KKGHVLSEYEGMSVT-----QCKSEDRSSSGPP	1301
2003	Db	ISLRRKFLNGLEPENITHMIGSMTIDCLGILNDLSDCEDKLPPIGYQCS-----	2051
1302	Qy	HETAAPKRTYDMGRVGRAISSASTEGLMGRAIPPERHSPHLLKEQHHIRGSIQTGIPR	1361
2052	Db	-----RVVWSTTDARKRCVYCKIVECPVPVEPDINSTVEHDENRTIAHS-----PT	2099
1362	Qy	SYVEAQEDYLRREAKLLKREGTPPPPPSRDLTEAY-----KTOALGPLKLKPAH	1411
2100	Db	SFTESSKESQNTAEIIS--PPSPDRPHSQTSGCYVHVLSKVPRITPSYSPQRSFGC	2158
1412	Qy	EGLVATVKEAGRSIHIPRELRHTPELPLAPPLKEGSITQGTPLKYDTGASTTGSKKH	1471
2159	Db	RPL-----PSAG-----SPTPTTHEIVTVGDPL--LSSGLRSIGSRRH	2194
1472	Qy	DVPSLIGSPRTFPPVHPPLDVMADARALERACVEE--SLKSRPCTASSSGSARGAPVIV	1530
2195	Db	STSSL--SPORS-----KURIMSPMTGNTYSRNNVSSVSTGTAT-----DLESSAKVD	2243
1531	Qy	PELGKPRQSPLYEDHCAPPA-----GHLPRGSPVTMREPTPRLOEGSLSSS	1577
2244	Db	HVLG-PLN5STSLGQNTSTSNLQRTVTVGNKNSHLDGSSSEMKSQSSADLVSKSSSL	2302
1578	Qy	KASQDKRLTSTPREIAKSPHSTVPEHHHPHPISEYHLLRGVSGVDLYRSHIPLAFDPTSI	1637
2303	Db	KGEKTVLGSKSSE--GSAHNVAYGP-klAPQVH---NTTSRELNVSKIGSFAEPSSV	2356
1638	Qy	PRGIPLDAAAAYLPRHLAPNPTYPHLYPPYLIRGY-----PD-----	1675
2357	Db	-----SFSSKRAL-----SFPPLH-----LRQQRNDRDQHTDSTQSANSPDEDETEV	2398
1676	Qy	-----TAALENRQTIINDYI-----TSQQMHN-----	1698
2399	Db	KTLKLSGMSNRSSIINEHMGSSRRDRQKKGKCKETFEKEKHSKSFLEPGQVTTGEGN	2458
1699	Qy	-----TATAMAQR-----ADWL--RGLS-----PRESS	1719
2459	Db	LKPEFMDVLTPEYMGORPCNNVSSSKIDGKLSMFCVPKAPMQVSGSAKELQAPKRRT	2518

Db 479 -EMVSGYVCEGDHKTMAKIDR-----VSLIK-----RKREQQLVR 516
QY 667 QOHKLWKEKERNARRKKKA-----PAAASEEAAFPVPVEDEEASG 709
Db 517 EOEKKKQBESSLUKQVEQSSASQTGIKOLPSASTGIPASTASVSTQVEPEEA-- 574
QY 710 VSGNEEMVEEABALHASGNEVPRGCSGPATVN--NSDTEIPSPHTEAAKDTQONGP 767
Db 575 -DQHQQLOVQOPISVLSDGTVDGSGSVFTESRVSSQOVTYSGQH-EQAHSTGTVP 632
QY 768 KPATLGAAGPPPPPTPPRRTSRARIEPTPASEA-TGAPTPPPAPPSAPPPVPVKE 826
Db 633 HIPSTVQAOSQPHG-VYPSSVAQSQSQSPSSSLTGV-----SSQPIQHQQ 681
QY 827 KBEETAAAPVBERGEQKPAABELAVDTCKAEPVKSECTEABEGPAKGDAAEAT 886
Db 682 QQIQQTAPP-----QQT 694
QY 887 AEGALKAKEKGGSGRATTAKSSGAPQSDSSATCSADEVDEAEGDKNRLSPRSLIT 946
Db 695 VQYSL---SQTSTSSRATTAAQPVSPQ-----718
QY 947 PTGDPANASPKPLDLKQKQAAAIPIQVTKVHEPPREDAAATPKPAPPAPPQNLO 1006
Db 719 -----APO-----VLPQVSAGKQGFPR-----LPPQVPGDSNIA 748
QY 1007 PESDAPQPGSSPRGKSRSPAPPADKEAFAAEAKLPGDPCWTSGLPFPVPREVIKAS 1066
Db 749 PSSNVA-----VCIHSTVLXPMPTEVL-----772
QY 1067 PHAPDPSAFSYPAGPHPLGLHDTARPLVPRPTISNPPPLISSAKHPSVLERTIGATS 1126
Db 773 -----ATPGY-----FPTVQVQVYESN-----LLVPMGGV- 797
QY 1127 QGMSVOLHPYSEHAKAPVGTMLPLMDPKLAPFGVKQEQLSPRGQAGPPESLGV 1186
Db 798 -GGQVQVSPGSLAQAPTSSQAV-----LESTQGV-----SQVAPAEFVAV 840
QY 1187 -----PTAQAEASVLRTGALGSPVCGSITKGPSTRVPSDSAITYRGSITHTPADVLY 1239
Db 841 AQOATQPTTLASSV--DGAHSDVASG-MSDG--NENVPSSG-----RH 880
QY 1240 KGTITRIIGEDSPRLDRGREDSPKGVHIYEGKGHVLSEYGMVSTQCSKE-----1292
Db 881 EGRITKRHYKSVRSRSRHEKTSRPKRLILVNSKGD-----RVVECOLETHNRKAV 932
QY 1293 -----DGRSSGPPHETAAKRTYDMGRVGRRAISSASIEGLMGRATPPERHSPHLK 1346
Db 933 TKFDLGDGN-----PEEITIMVNNDFI-----LAIERESFVDQVREII---EKADEMLS 980
QY 1347 EQHHIRGSITQIGIPRSYVEAQEDYLRRKALKREGTPPPPPPSRDLTEAYKTQALGPLK 1406
Db 981 EDVSVEPEGDQGL--ESLQKDDYGFSGQKLEGEFKQIPASSM-----PQQ 1026
QY 1407 LKPAHEGLVATYKAGRS--IHEIPRELRHTPELAPRPLKEGSIQTGLKYDTGAS 1464
Db 1027 IGIPTSLSLQVHVSAGRRFIVSPBSRLRESKVFP-----SEIT-----DTVAA 1071
QY 1465 TTGSK-----KHDVRSI-----IGSQRTFPFVHPHLDVWAD 1495
Db 1072 STAQSPGMNLSHSASSLISLQAFSELRRRAQMTGEPNTAPNFSHTGPTFPVVPV-- 1125
QY 1496 ARALERACYEESLKRPGTASSGSGSIARGAP-----VIVPELGKPRQSPL--TYEDH 1546
Db 1126 -----FLSIAGVPTTAATAPATVPATISSPNDISTSVIOSEVTVPTEEGIAGVATST 1177
QY 1547 GAPPAGHLPRGSPVTWRETPRLQEGSLSSKASQDRKLTSTPREIA---KSPHSTVPEH 1603
Db 1178 GVVTSGL-----PIPPVSESPVLSVSSVSS-----ITIPAVVSTSTSPSLQVPTS 1223
QY 1604 HPHPISPYELLRGVSGVDLYESHIPLAFDPTSIPRGIPLDAAAYLLPRHLAPNPTYPH 1663

Db 1224 TSEIV-----VSSTALYPS-----VTVSATASAGGSTATPGPK--- 1257
QY 1664 LYPPVLI-----RGYPTDALENRO-----TIINDYIT 1691
Db 1258 --PPAVVSOQAAGSTTVGATLTSVSTTTTFPSTASQLSIQSSSTSTPLAETVVVSAHS 1315
QY 1692 SQOMHNTATAMA-----QRADMLRGLSPR-----ESSIALNVAACP 1728
Db 1316 LDKTSHSITGLAFSLASAPSSSSSGAGVSSVISQPGGLHPLVIVSVTASTPILQOAGP 1375
QY 1729 RGIIDLSQVPHLPVLVPTPGTPATMDRLAYLPTAPOPFSSRHSSSPSPGPG--THLTK 1787
Db 1376 TSTPLLPQVSPSPPLVQPVANVPV---QOTLIHSQPP-----ALLPNQPHTHCP- 1423
QY 1788 PTTTSSSERDRDRDRDREREKSLTSTTTTVEHAPLWRPGTEQSSGSSSSGGGGS 1847
Db 1424 -----EVDSDTQPKAPGIDDIKILEE-----KLSJLFSHSSGA--- 1458
QY 1848 SSRPASHSHAHQHSPISPRTQDALQORPSVLHNTQMKGI-ITAVBPSPKPTVLRSTSTSSP 1906
Db 1459 -----QHASVSLETS-----LVIESTVTPGPTTAVAPSK--LITSIT--- 1494
QY 1907 VRPAATFPFPAHCPILGGLDGVVPTLMBPVLLPKBAPRVARPERPRADTGHAFKAPPAR 1966
Db 1495 -----STCLPPTNLPLG-----TVALPVTVPVTPGVSTPVSTTT 1529
QY 1967 SGLPASPSKSGSEPRPLVPPVSGHATARTPAKNLA PHASPDPPAPASADPHREKT 2026
Db 1530 SVKRGTPAPSKPLTKAPVLPVGTBLPAGTLPSEQ-----PPFGPSL---T 1574
QY 2027 QS-KPFSIQEILRLSLYHSGSYSPGVEPVSPVSPSLTHDKGLPKHLELDKSLGE 2085
Db 1575 QSQQPLEDLDAQLR-----RTLSPEXITVTSV-----1602
QY 2086 LRPKQGPVKLGGEAAHPLHRLPLPE---SQSSSPLIQTAPGV---KGHORVVTLAQH 2138
Db 1603 -----GPFVMAAPTA-ITEAGTQPKGVQVKEGFLATSSGAGVFKMGRFQVSVAA-- 1653
QY 2139 ISEVITQDYTRHPPOOLSAPLPAPLYSPFGASCPVLDLRRRPPSDLYLPPP----- 2188
Db 1654 -----DGAQKEGKNKSEDAKSVHFESESTSESSVSSSESTLVKPEPNIITPGISS 1706
QY 2189 DHGAPARGSPHSEGGKRSPEPNKTS-----VLGGGEDGIE-----PVSP 2228
Db 1707 DVPESAHKTASEAKSDGTQPTKGRFQVTTTANKVGRFSVSKTBDKITDTKKEGVASP 1766
QY 2229 EGWTEPGHSRANVYLLYRDGEOTEPSRMGSKSPGNTSQP-PAPFSKLTESNAMVSKK 2287
Db 1767 PFMDLEQAVLPAVITPKKPK-ELSEPSHLN-----GPSSDPEAAFLSRDVGSGSPHSPH 1821
QY 2288 QBINKKLATHNRNEPEYNISQPTGTEIFNNPAITGTGLMTYRSQAVQ-----EHAFTN 2339
Db 1822 QLSKSL-----PSQNLSQLSNFSNYSNWSNEDIEDDLKELRLRDLKHLKEI 1874
QY 2340 MGLEAIIRKALMGKYDOWEESPPISANAFNPLNASISLPAAMPITAAADGRSDHTLTSPGG 2399
Db 1875 QDLOSROKHEIESLYTLKGVKPP-----AVIIPPAAPLS---GRRRRPTKS--- 1917
QY 2400 GGAQVSGRPSRRAKSP-APGLASGDRPPV-----SSVHSEGD 2438
Db 1918 --KGSKSRSSSLGNKSPQLSGNLSGQSAASVLHPHQTLHPFGN 1959

RESULT 44

US-09-854-856-10
; Sequence 10, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Doncho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides

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; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 2092
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2092)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-10

Query Match      2.8%; Score 369.5; DB 4; Length 2092;
Best Local Similarity 18.7%; Pred. No. 1.2e-12;
Matches 479; Conservative 285; Mismatches 885; Indels 915; Gaps 106;

QY 147 PVSPPSPHTDPELELVPRLSKEELIQNMDRVDRITWVEQIQSKLKKKQOQLBEEAAK 206
DB 99 PLSLPQPSIPAAVPQAPPEPHEETV-----TATATSQVAQPPAAAPAEQOAVA 149
QY 207 PPEP-----EKVSPPPPIESKHSLSVQIIYDENRKAEEAAHRIELGLGPQVELPLY 257
DB 150 GRAPSTVPSTSKDRVPQPSL-----VGSKEEPPPA 181
QY 258 NQPSDTRQYHENIKINOAMRKILYFKRNHARKQWKQFCQRYDOLMEALEKKYERIE 317
DB 182 RSGSG-----GGSAKEPQBERSQQDDI-ELEETKAVGMS 215
QY 318 NNPRRAKESKV-REYEQKQPIRQKQ-----ELQRMQSRVQQRGSLMSAARSE 369
DB 216 NDRFLKFDIEIGRQFKTYKGLDTEITVEVAMCLODRK-----LTKSERQRF 265
QY 370 HEVSEIIDGLSEQENLEKQMRQLAVIPPMYLDADQORIK-----FINNGLM-ADPMKVYK 424
DB 266 KBAEMLKGL-QHPNIVR-----FYDSWESTVKGKICVILVTELMSTGLTKYL 313
QY 425 DR-----QMMNWSQEKETFEKFMQHPK-----NFGLIA 455
DB 314 KRPFKWKIKVLRSCWQQLKGLQFLHTRTPPIIHRDLKCDNIFITGTSVKIGDLGL-- 371
QY 456 SFLEKRTVAECVL-----YYLTKQENY-----KSLVRSYRRRGSKSQOQOQQQ 501
DB 372 ATLKRASFQKSVIGTFEFMAPEYBEKYDESDVDVYAFGMCMELEMATSEYPYSECQNAQI 431
QY 502 QOQOQOQOQP-----MPRSSQ-----EEKDEKEKEAKEEKEPEVENDKEDLLK 547
DB 432 YRRTSGVFPASFDKVAIPEVKELIIEGCIQNKQDERYSIKOLLNHAFFQOETGVRVELAE 491
QY 548 EKTDDTSGEDNDKEAVAGKRKTANSQGRKGRITRSMANEANSE-EAITPQOQSAELAS 606
DB 492 E-----DDGEKIAIKLWLRIEDIKLKGKYNKNEAIEFSLDERDVPEDVAQ--- 538
QY 607 MELNESSRWTEEMETAKKGLLEHGRNWSAIARMVGSKTYSQCKNFYNYKKQNLDEIL 666
DB 539 -EMVESGYCEGDHKTMAKIDR-----VSLIK-----RKREQQLVR 576
QY 667 QOHLKWEKERNARRKKKA-----PAAASEEAAFPVPVVEEEMEASG 709
DB 577 EGEKKKQKQESSLKQOQVQSSASQGTGKQLPSASTGIPASTTSASVSTQVEEPEEA-- 634
QY 710 VSGNEEMVEEAEALHASGNEVPRGCSGPATVN--NSSDTEISIPGPTHEAAKDTQONGP 767
DB 635 -DQHQQLQYQPSISVLSDDGTVDSQGSVFTESRVSSQQTYSYGQH-EQAHSTGTVP 692
QY 768 KPPATLGADGPPGPTTPPTARTSRAPIETPASEA-TGAPTPPPAPSPSPAPPPVVKEE 826
DB 693 HIPSTVQAOQPHG-VYPPSSVAQSQSQGQSSSLTGV-----SSSQIHPHQ 741
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QY 827 KEEETAAAPPVBEGBEQPPAAAEALAVDTGKAEPEPVKSECTEEAEERPAKGDAEAEAT 886
DB 742 QOQIQQTAPP-----QQT 754
QY 887 AEGALKAKEKGGSGRATTAKSSGAPQDSDSSATCSADEVDEAGGDKNRLLSPRSLLT 946
DB 755 VQYSL---SQTSTSEATTAQPVSPQ----- 778
QY 947 PTGDPANASPOKPLDLKQLKQRAAAIPIQVTKVHEPPREDAATPKPAPPAPPQNLQ 1006
DB 779 -----APO-----VLPOVSACKQGFPR-----LPPQVPGUSNIA 808
QY 1007 PESDAPQPGSSPRGKSRSPAPPADKEAFAAEQKLPGDPPCWTSGLPFPVPPREVIKAS 1066
DB 809 PSSNVAS-----VCIHSTVLXPPMPTVL--- 832
QY 1067 PHAPDPSAFSAPPQHPHPLPLGLHDTARPVLPPTTISNPPPLISSAKHSVLERQIGATS 1126
DB 833 -----ATPGY-----FPTVVOPIYESN-----LIVPMGGV- 857
QY 1127 QGMSVOLHVYPSEHAKAPVGTMTGLPMDPKLAPFSGVKQEQQLSPRQOAGPPPSLGV 1186
DB 858 -GGQVQVSPQGSGLAQAPTSSQAV-----LESTQGV-----SQVAPAPPAV 900
QY 1187 -----PTAQBASVLRGTALGSPGGSITKGIPTSRVPSDSAITYRGSITHGTADVLV 1239
DB 901 AQOATQPTTLASSV--DSAHSADVAG-MSDG--NENVPSSSG-----RH 940
QY 1240 KGTITRIIGEDSRLDRGREDSLPKGHVHYEGKGHVLSYEGGMSVTQCSKE----- 1292
DB 941 EGRITTKRHYKSVRSRSHKTSRPKRLILNVSNGD-----RVVECOLETHNRKMV 992
QY 1293 -----DGRSSGPPHETAAKRTYDMMEGRVGRJASSAIEGLMGRAIYPERHSPHLK 1346
DB 993 TKFIDLQGN-----PEIATIMVNDPI-----LAIERESFVQVREIL---EKADEMLS 1040
QY 1347 EOHIRGISTOGIPRSPYEAQEDYLRRKAKLKEGTPPPPPSRDLTAYKTQALGPLK 1406
DB 1041 EDVSVEPEGDQGL--ESLOGKDDYGFSGQKLEGEFKQPIPASSM-----PQ 1086
QY 1407 LKPAHEGLVATVKEAGRS--IHIEIPREELRHTELPPLAPRPLKEGSIQTGTPLKYDTGAS 1464
DB 1087 IGITPSSLTQVHVSAGRREIVSPVESRLRESKVFP-----SEIT-----DTVAA 1131
QY 1465 TTGSK-----KHDVRSL-----IGSGRTTTPPVHPLDVMAD 1495
DB 1132 STAQSPGMNLSHASLSLQOAFSELRRRAQMTGPNTPNFSHTGTPTFPVVP----- 1185
QY 1496 ARALERACYEBSLKSRPGTASSGSGSIARGAP-----VIVPELKGPRQSP--TYEDH 1546
DB 1186 -----FLSSIAGVPTTAAATAPVPATSSPPNDISTSVIQSEVTVPTEEGIAGVATST 1237
QY 1547 GAPPAGHLPRGSPVTWREPTPLQEGSLSSSKASQDKLTSTPRETA---KSPHSTVPEH 1603
DB 1238 GVVTSGGL-----BIPPVSESPVLSVSSVSS---ITIPAVVSIITSTPSLSQVPTS 1283
QY 1604 HHPISPYEHLRGVSGVDLYRSHIPLAFDPTSIPIRGIPLDAAAAYVLPRLHAPNPTYPH 1663
DB 1284 TSEIV-----VSSTALYPS-----VVVSATSASAGSGSTATPGPK--- 1317
QY 1664 LYPPVYLI-----RGYPDTAALENRQ-----TIINDYIT 1691
DB 1318 --PPAVVSQQAAGSTTVGATLTSVSTTTFSPSTASQLSLSSTSTPTLAEIVVVAHS 1375
QY 1692 SQOMHNTATAMA-----QRADMLRGLSPR-----ESSLALNVAAGP 1728
DB 1376 LDKTSHSTTGLAFSLAPSSSSSGAGVSSVYSIQFGLHPLVIPSVIASPTILPOAAGP 1435
QY 1729 RGIIDLQVPHLPVLPVPTPGTATAMDRLAVLPTAQOPFSSRRHSSSPSPGPG-THLTK 1787
DB 1436 TSTPLLPVQVPSIPPLVQPVANPAV---QOTLIHSQFQP-----ALLNQPHTHCP- 1483
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QY 1788 PTTSSSERDRDRDREREKSLTSTTTTVERHAPIWRPGTEOSSSGSGSGGGGGS 1847
Db 1484 -----EVDSDTQPKAGCIDDDIKTLEE-----KLRSLFSEHSSGA--- 1518
QY 1848 SSRPASHAHQHSPISPTQDALQORPSVHNTGMMKI-ITAVEPSKPTVLRSTSTSP 1906
Db 1519 -----QHASVSLETS-----LVIESTVTPIGITTAVAPSK--LITSTT--- 1554
QY 1907 VRPAATPPATHCPGLGTTGVTLMPEVLLPKAPRVARPERPRADTGHAFKAPPAR 1966
Db 1555 -----STCLPTNLPLG-----TVALPVTVPVTPQGVSTPVTSTT 1589
QY 1967 SGLPEASSPSKSGSEPLVPVPSGHATARTAKNLAPHASDPDPAPPASADPHREKT 2026
Db 1590 SGVKPGTAPSKPLTKAPVLPVGTLPAGTLPSEQL-----PPFGPSL---T 1634
QY 2027 QS-KPFSIQLELRSLGYHSSVSPGVEVPVSPVSPSLTHDKGLPKHLEELDKSHLEGE 2085
Db 1635 QSOQPLEDLDAQLR-----RTLSPXITVTSAV----- 1662
QY 2086 LRPKQPGVKLGCEAAHPLHLPLPE---SQPSSSPLLOTAPGV---KGHQRVVVTLAQH 2138
Db 1663 -----GPVSMAPTA-ITBAGTQPKQSVQVKEGVLATSSAGVFKMGRFOVSVAA-- 1713
QY 2139 ISEVITQDVTYRHHPOQLSAPLAPLYSPFGASCPLVLDLRRPPSDLYLPPP----- 2188
Db 1714 -----DGAQKEGKNKSEDAKSVHFESSTSESSVSSSPSTLVKPEPNGITIPGISS 1766
QY 2189 DHGAPARGSPHSGGKRSPEPNTKS-----VLGGEGEGIE-----PVSP 2228
Db 1767 DVPESAHTKTASBAKSDTOPTKVGRFOVTTANKVGRFSVSKTEDKITDTTKKEGVPASP 1826
QY 2229 EGMTEPCHRSAYVPLLYRDGEOTEPSRMGSKSPGNTSOP-PAFFSKLTESNAMYKSK 2287
Db 1827 PFMDLQAVLPVPIKKEP-ELSEFSLN-----GFSSDEAPFLSRDVEDDGGSPHSPH 1881
QY 2288 QEINKKLNTHRNEPYNISQPGTEIFNMPAITGTGLMTYRQAVQ-----EHASTN 2339
Db 1882 QLSSKSL-----PSQNLQSLSNFSNGSSDNESDIEDDLKLEURLRLDKHLKEI 1934
QY 2340 MGLEAIRKALMKYQDWEESPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPOG 2399
Db 1935 QDLQSQKHIEISLYTKLGKVP-----AVIIPPAAPLS-----GRRRPTKS---- 1977
QY 2400 GKGAKVSGRPSRRKAKSP-APGLASGDRPPSV-----SSVHSEGD 2438
Db 1978 --KGSKSRSSSLGNKSPQLSGLNSQSAASVHLHPQOOLHPPGN 2019

RESULT 45
US-09-854-856-40
; Sequence 40, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 2169
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
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; LOCATION: (1)...(2169)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-40
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Query Match      2.8%; Score 369.5; DB 4; Length 2169;
Best Local Similarity 18.7%; Pred. No. 1.2e-12;
Matches 479; Conservative 285; Mismatches 885; Indels 915; Gaps 106;
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QY 147 FVSPSPPTHTDELELVPPRLSKBELIQMMDRVDRBITVVEQOISKLKKKQOOLBEEAAK 206
Db 39 PLSLPQPSIPAAVPOSAPEPPEHRETV-----TATATQVAQPPAAAPGEQAVA 89
QY 207 PPEP-----EKVSPPTTESKHSILVQIYYDENRKKAAAHRLBGLGPGVPELPLY 257
Db 90 GAPSTVPSSTSKDRPVQPSL-----VSGKEEPPPA 121
QY 258 NOPSPDTQYHENIKINQAMRKLIIFYKRRNHARKQWKQFCORYDQLMLEAKKVERIE 317
Db 122 RSGSG-----GGSAPQPEERSQOQDDI--EELTKAVGMS 155
QY 318 NNPRRAKESKV-REYYEKQPFPIRKOR-----ELQERMOSRVGQSGSLMSAAARSE 369
Db 156 NDRFLKFDIEIGRSGSFVTVYKGLDTEFTVEVAMCELDQRK-----LTKSERQRF 205
QY 370 HEVSEIIDGLSQENLEKQMRQLAVIPPMYLDADQORIK---FINMGLM-ADPMKVYK 424
Db 206 KEAEMLKGL-CHPNIVR-----FYDSWESTVKKKCVILVTELTSGTLKIYL 253
QY 425 DR-----QVMMWSEQKEKTFREKFMQHPK-----NFGFLTA 455
Db 254 KRFFVKWKIKVLRSMWCRQILKGLQFLHTPTPIIHRDLKCDNIFITGPTGVSVKIGDLGL-- 311
QY 456 SFLERKTVAEVL-----YYVLTKNENY-----KSLVRRSYRRRGKSCQOQOQOQ 501
Db 312 ATLKRASFAKSVIGTPFERMAPBMEBEKYDSDVYAFGWCMLEMATSYBPYSECQNAAQI 371
QY 502 QOQOQOQOQP-----MPSRSG-----BEKDEKEKEKEAEKEEKEPEVENDKEDLLK 547
Db 372 YRRVTSVGVKPAFDFKVAIPEVKEIIEGCIQNKDERYSIKOLLNHAFFQEEGTGVVELAE 431
QY 548 EKTDDTSGEDNDEKAVASKGRKTANSQGRKRITRSMANEANSE-EAITPQQSAELAS 606
Db 432 E-----DDGEKIAIKLWLRIEDIKLGKYKNEAIEFSPDLERDVEDVDAQ--- 478
QY 607 MELNESSRWTEEMETAKGLLEHGRNWSALARVGVSKTVQCKNFYFNKYKQNLDEL 666
Db 479 -EMVESGVCEGDHKTMAKAIKDR-----VSLIK-----RKREQQLIVR 516
QY 667 QQHKLMEKERNARRKKKA-----PAAASEEAAFPVVEDEMEASG 709
Db 517 EEQEKKKQEESSLKQOVESASQTIKQLPSASTGIFTASTTSASVSTQVEPEPEA-- 574
QY 710 VSGNEEEMVBERAEALHAGSNEVPREGCSGPATVN--NSSDTEIPSPHTEAAKDTGQNGP 767
Db 575 -DQHOQLQYQOFSISVLSDGTVDSCGSSVFTESRVSSQOQTVSYGSOH-EQAHSTGTVP 632
QY 768 KPAPTLGADGPPGPPPTPRRTSRAPIEPTASEA-TGAPTPPPAPPSAPPPVPVPEE 826
Db 633 HIPSTVQOSQPHG-VYFPSSVAQSQSQSQSSSLTGV-----SSQPLQHQQ 681
QY 827 KEEETAAAPVVEEGESEQPPAAEELAVDTGKAEFPVKSECTEAEPEGKAGKDAEABAT 886
Db 682 QQGIQQTAPP-----QQT 694
QY 887 AEGALKAEKKGSGGRATTAKSSGAPQSDSATCSADEVDEAEGGDKNRLSPRPSLLT 946
Db 695 VOYSL---SQTSTSEATTAQFVSQOQ----- 718
QY 947 PTGDPANASPKPLDLKQLKQRAAAIPIQVTKVHEPPREDAAFTKPAAPPAPPONLQ 1006
Db 719 -----APQ-----VLPQVSAKGQGFPR-----LPQYFGDSNIA 748
QY 1007 PESDAPQPGSGSPRKSRSAPPADKFAFAEAKLPGDPPCWTSGLPFPVPPREVIKAS 1066
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Db 150 GPAPSTVPSSTKDRPVSPSL-----VGSKEPPPPA 181
QY 258 NQSDTRQYHENIKINQAMREKLLILYKRENHARKQWKFCORYDOLMEALEKKVERIE 317
Db 182 RSGSG-----GGSAPQEBERSQOQDDI-EELETKAVGMS 215
QY 318 NNPRRAKESKV-REYVEKQFFBIRKQ-----ELQERMQRVQGRGSLSMSAARSE 369
Db 216 NDGRFLKFDIEIGRGSFKTVYKGLDTETTVAVWCELQDRK-----LTKSERQRF 265
QY 370 HEVSEIIDGLSEBENLEKQMRQLAVIPMLYDADQORIK-----FINNGLM-ADPMKVYK 424
Db 266 KEAEMLKGL-ORHPNTIVR-----FYDSWESTVKKKCIVLVTELMTSGTLKTYL 313
QY 425 DR-----QVMNWSQEKETPREKFMQHPK-----NGLITA 455
Db 314 KRFKWKIVLRWCQOILKGLFLHTRTPPIIHRDLKDNITITGPTGSVKIGDLGL-- 371
QY 456 SFLEKTVABCVL-----YYLTKQENY-----KSLVRRSYRRRGKSQOQOQOQ 501
Db 372 ATLKRASFASKVIGTFEFMAPEMYEYKDESVDVYAFGCMLEWATSEYFYSECQNAOI 431
QY 502 QOQOQOQOQ-----MPRSSQ-----EKKDEKEKEKEBEKEBEVENKEDILK 547
Db 432 YRRVTGVKPAFDKVAIPEVKIEIEGICRQNKDERYSIKDLNHAFFQOETGVRVELAE 491
QY 548 EKTDDTSGEDNDEKAVASGRKTANSQGRKGRITRSMANEANS-BAITPOQSAELAS 606
Db 492 E-----DGEKIAIKLWRIEDIKLKGKYKDNIAIEFSFLERDVEDVAQ----- 538
QY 607 MELNESRWTEEBMETAKKGLLEHGRNWSAIAIRMVGSKTVSQCKNFYFNKYQRNLDLIL 666
Db 539 -EMVESGYVCEGDHKTMAKIDR-----VSLIK-----RKREQQLVR 576
QY 667 QOHLKWEKERNARRKKKA-----PAAASEEAAFPVPVEDEMEASG 709
Db 577 EOEKKKKQESSLUKQVEOSSQSGQIGIKQLPSASTGIPTASTSASVSTQVEPEPEA-- 634
QY 710 VSGNEEMVEEABALHASGNEVPRGCSGPATVN--NSSDTEISIPSPHTEAAKDTGONGP 767
Db 635 -DQHQLQYQOQPSISVLSDGTVDGSGSVFTESRVSSQOQTVYSGQH-EQASHGTGTPG 692
QY 768 KPATLGAQGGPPPTPPRRTSRAPIETPASEA-TGAPTTPPAPPSAPPPVVPKBE 826
Db 693 HIPSTVQAQSGPHG-VYPPSSVAQSQSQOQSSSLTGV-----SSQOIHPQO 741
QY 827 KBEETAAPVVEGEBQKPPAAELAVDTGKAEHPVKSECTBEAEGPAKGDAAEAAT 886
Db 742 QOQIQQTAPP-----QQT 754
QY 887 AEGALKAKEKGGSGRATTAKSSGAPQDSQSSATCSADEVDEAEGDKNRLLSRPSLIIT 946
Db 755 VQVSL--SQTSTSSSEATTAPVQSQO----- 778
QY 947 PTGDFRANASPKPLDLKQORAAIPIQVTKVHEPPREDAAPTKAPAPPAPPQNLQ 1006
Db 779 -----APQ-----VLPQVSAQKQGFPR-----LPPQVPGDSNIA 808
QY 1007 PESDAPQOQSGSPRGKRSRSPAPADKEAFAAEAKQLPGDPPCWTSGLPPVPVPRVIKAS 1066
Db 809 PSNVAS-----VCIHSTVLKXPMPTTEVL----- 832
QY 1067 PHAPDPSAFSAPPQGHPLPLGLHDTARVLPVPRPTISNPPPLISSAKHPSVLEROIGAIS 1126
Db 833 -----ATPGV-----FPTVQPYVESN-----LLVPMGGV- 857
QY 1127 QGMSVOLHVPYSEHAKAPVGTMTGLPLPMDPKLAPFGSVKQEQOLSPRGQAGPESLGV 1186
Db 858 -GGQVQVSGFGLAQAPTSSQOAV-----LESTQGV-----SQVAPAEPAV 900
QY 1187 -----PTAQEASVLRGTALSGVPGSITKGIPSTRVPSDSAITYRGSITHTGTPADVLY 1239
Db 901 AQOQATQPTTLASSV--DSAHSDVASG-MSDG--NENVPSSG-----RH 940

QY 1240 KGTITRIIGEDSPRLDRGREDSLPKGHVVIYEGKKGHVLSYEGGMSVTOCSKE----- 1292
Db 941 EGRITTKRHYKVRGRSRHEKTSRPKLRIILVNSNGD-----RVVECOLETHNRKMV 992
QY 1293 -----DGRSSSGPPHETAAPKRTYDMMBGRVGRRAISSASIEGLMGRAIIPPERHSPHLK 1346
Db 993 TKFDFLDGDN-----PEEATIMVNDFI-----LAIERESFVDQVREII---EKADMLS 1040
QY 1347 EOHIRGISTQIGIPRSYVBAQEDYLRRKALKRGTGTPPPPPPSRDLTAYKTQALGPLK 1406
Db 1041 EDVSVEPEGDQGL--ESLQKDDYGFSGQKLEGFQKQIPASSM-----PQO 1086
QY 1407 LKPAHEGLVATYKEAGRS--IHEIPREELRHPTPELAPRPLKEGSIITQGTPLKYDVTGAS 1464
Db 1087 IGITPSSLTQVVHVSAGRRFIVSPVPSRLRESKVFP-----SEIT-----DTVAA 1131
QY 1465 TTGSK-----KIDVRSL-----IGSPRTFPPVHPLDVMD 1495
Db 1132 STAQSPGNLSSHASLSLQQAFSELRAQMTGEGTAPPNFSHTGTPFPVVP----- 1185
QY 1496 ARALERACYEELKSRPGTASSSGSAGAP-----VIVPELGKPRQSPL--TYEDH 1546
Db 1186 -----FLSSIAGVPTTAAATAPVPATSSPPNDISTSVIQSEVTVPTTEGIAGVATST 1237
QY 1547 GAPPAGHLPRGSPVTRBPTPELOGLSSSSKASQDKLTSTPREIA---KSPHSTVPEH 1603
Db 1238 GUVTSGGGL-----PIPVSESPVLSVVSS-----ITIPAVVSISTSPSLOVPTS 1283
QY 1604 HPHPISPVEHLRGVGDVLYRSHIPLAFDPTSPRGIPLDAAAAYILPRHIAPIPTVPH 1663
Db 1284 TSEIV-----VSSALYPS-----VTVSATSASAGSTATPGK-- 1317
QY 1664 LYPPYLI-----RGYDPTAALENRQ-----TIINDYIT 1691
Db 1318 --PPAVVSOQAAGSTVGCATLTSVSTTTSPFSTASQLSQSSSTSTPTLAETVVVSAHS 1375
QY 1692 SQOMHNTATAMA-----QRADMLRGLSPR-----ESSLALNVAAGP 1728
Db 1376 LDKTSHSSTTGLAFSLASAPSSSSSGAGVSSVISOPGGLHPLVIPSVTASTPILQOAGP 1435
QY 1729 RGIIDLQVPHLVLVPTTGTPTAMDRLAYLPTAPOFFSSRSHSSSPLSGGP-THLTK 1787
Db 1436 TSTPLLPQVPSIPPLVQPVANVAV--QOTLIHSQOP-----ALLNPHTHCP- 1483
QY 1788 PTTTSSSERDRDRDREREKSIILSTITVEHAPIWRPGTEQSSGSSSSSGSGGS 1847
Db 1484 -----EVDSDTQPKAPGIDDKTLEE-----KURSLFSEHSSGA-- 1518
QY 1848 SSRPASHSHAHQHSPISPRTQDALQORPSVLHNTGMKGI-ITAVEPSKPTVLRSTSTSSP 1906
Db 1519 -----QHASVSLETS-----LVIESITVPGIPITAVAPSK--LLTSTT-- 1554
QY 1907 VRPAATFPPTHCPILGGTLDGVYPTLMEPVLLPKAPRVARPERPRADTGHAFKAPPAR 1966
Db 1555 -----STCLPPTNPLIG-----TVALPVTVPVTPGVSTPVSTTT 1589
QY 1967 SGLEPASSPSKSGSERPLVPPVSGHATARTPAKNLA PHASPOPPAPASADPHREKT 2026
Db 1590 SGVRPGTAPSPPLTKAPVLPGTLPAGTLPSEOL-----PPFPGPSL----- 1634
QY 2027 QS-KPFSTIQEELRSLRGVHSGSYSGPEGVPSVSSPSLTHDKGLPKHLELDKSLRGE 2085
Db 1635 SQOQPLEDLDAQLR-----RTLSPXITVTSVAV----- 1662
QY 2086 LRPQKQGVKLGGEAAHPLPHLRPLPE---SQPSSSPLLOTAPGV-----KGHORVVTLAQH 2138
Db 1663 -----GFSVMAAPTA-ITEAGTQPKGVSVKXGCVLATSSGAGVFGVGRFOVSVA-- 1713
QY 2139 ISEVITQDTRHHPQOLSAPLPAPLYSPFGASCPLDLRLRRPPSDLYLPPP----- 2188
Db 1714 -----DQAQKEGKNKSEDAKSVHFSSTSESSVLSSSSPESTLVKPEPNTIPIGSS 1766

Db 568 GPA-----GPRGANGAPGNDGAKG-----DAG-----APGAP---594
QY 1446 LKEGSIQTGTP-----LKYDTGASTTGSKKHD-----VRLIGSPGR-----TFF---PVH 1488
Db 595 ---GS---QCAPGLQGMPPGERGAAGLPCPKGDRDAGPKGADGSPGKDGVRGLTGPIGPPG 649
QY 1489 PLDMADARALERACYEESLSKSPGTASSGSGIARGAPVIVDELKPKPROSPLTYEDHGA 1548
Db 650 PAGAPGD-----KBSGSPGSPAGPTGARGAPGDRGEPGP---GPAGFA---GP 692
QY 1549 PFAGHLPRGSPVTMRPTPLRLOGSLSSSKASQDRKLTSTPREIAKSPHSTVPEHHPHI 1608
Db 693 PGAD-----GQGAKEGPGDAGKGD-----AGPPGAPGAPGPGPI 729
QY 1609 -----SPYELLRGVGVDLVYRSHIPLAFDPTSIPIRGIPLDAAAYLPRHLAPNPTYPHL 1664
Db 730 GNVGAFGKAGSAGP-----PGATGPGGAAGRVGP---PGPS-GNA 768
QY 1665 YPPYLIRGVPDPTAALNRQTIINDYTSQOMHNTATAMAQRADML-----RGL 1713
Db 769 GPP-----GPPGAGKEGKGRGE-----TGPAGRPGEVGPVPPGPPGAGEKGS 812
QY 1714 SPRESSLALNYAAGRGIIIDLSOVPHLPVLVPPT--PGTPATAMDRLAYLPTAPQPPSSR 1771
Db 813 PGADGAPAGPTPEPQGIAGQGVVGLPGQGERGPPGLPGPSGE-----PGKQGPSGAS 867
QY 1772 HSSPSLSPGPGTHLTPTTSSSERDRDRDRDREREKSLTSTTTVEHAPIWRPPT 1831
Db 868 GERGPPGPMGPPGLAGPAGESGRE-----CAPGA 896
QY 1832 EGSSGSGSGSGGG-----GSSSRPASHAHQHSPIISPTQDALOORPSVLHNTQMKGI 1886
Db 897 EGSPGRDGSAGKGRGETGAPGPPGAXGAXGAPGVGP-----AGKSGD 941
QY 1887 ITAVEPSKPVLRSTSSPVRAATFPATHCPLGLTLDGVYPTLMPEVLLPKEAPRA 1946
Db 942 RGETGPAGP-----AGVGPAGARGP-----A 963
QY 1947 RPRPRADTGH-----AFLAKPPARSGLSPASSPSKSGSEPRPLVPPVSGH 1991
Db 964 GQGPGRDGETGEQDRTGKHRGFGLOGPPGPGSPCEQGPSASGP-----1013
QY 1992 ATTIARTAXNLAPHASPPDPAPASADPHREKTOSKPSIOELRLSIGVHGSSYSPE 2051
Db 1014 -----AGPRGPPGAGAPGKDGMLNGLPGPI-----GPPGPRGRTG 1048
QY 2052 GVEPVSPVSPSLTHDKGLPKHLEELDKSHLEGELRPKQGPVKLGEEAAHLPHLPLPE 2111
Db 1049 DAGFVGPVPPGPG-----PPGPPGPSAGDFDFSFLP-----1078
QY 2112 SQPSSSPLLTQAPGVKGHO-----RVVTLAQHISEVITQDYTR 2149
Db 1079 -QP-----POEAKHGGRYRADDANVVRDRLDLEVDVTLKLSQOENIRSEGRX 1128
QY 2150 HHPQQLSAPLAPLYFPAGSCVPLDLRRPPSLYLPDPDHGAPARGSPHSEGGKSPPEP 2209
Db 1129 KNPAR-----TC-RDLKMCCHSDW-----KSGEYWDIP 1154
QY 2210 NKTSVLGGEDGIEPVSPGEMTEPHGSRSAVYPLLYRDGEQTEPSRMG-----SKSPGN 2264
Db 1155 NQ-----GCLNDALIKVCNME-----TGTCVYV-----TOPSVAQKNWYISKPKD 1196
QY 2265 TSOPPAFFSKLTES-----NSAMVSKKQEKINKKLNTHNRNEPEYNIS 2307
Db 1197 KDRHVMFGSMTDGFOFEYGGQSDPADVAIQITFLRLMSTEASQNTTHCKNSVAYMQ 1256
QY 2308 QPG 2310
Db 1257 QTG 1259

RESULT 51

US-09-500-811-18

; Sequence 18, Application US/09500811
; Patent No. 6323314
; GENERAL INFORMATION:
; APPLICANT: Ovist, Per
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,811
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/187,319
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1341 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: COLLAGEN ALPHA 1 (I)
; US-09-500-811-18

Query Match 2.7%; Score 351; DB 4; Length 1341;
Best Local Similarity 20.1%; Pred. No. 7.7e-12;
Matches 350; Conservative 106; Mismatches 573; Indels 714; Gaps 81;

QY 722 EALHAGNEVPRGECGTPATVNNSDTESIPSPHTEAAK-DTCQNGPKPPA-TLGDGPP 779
Db 77 ETKNCFEAGVPEGECC-PVCPDGSSEPTDQETTVGVEGPKGDTGPRGPGAGPPGRDGP 135
QY 780 -----PGPTTPTRTSRAPITPASEATGATTP-----PA 811
Db 136 GQGLGPPGPP-----GPPGPGLGNGFAPQLYGYDEKSTGGISVPC 178
QY 812 PPSGAP-----PPVVPKEEKEEETAAAPVVEGE-----EQKPPAAEELAVDTGKA 858
Db 179 PMGSPGRLPGPPGAPGPGZGFZ---GPPGZPGZPGASGPMGPRGPPGPGKGBBGZA 234
QY 859 EEPVSKTEETAEAGKADAAEATAEAGALKAEKKGSGSRATTKSSGAPQSDSS 918
Db 235 GKPR-----PGZRGPPGPGZGARGLPFTA--GLPCMKGHRGFSGLBAGBAGPAG---283
QY 919 ATCSADEVDEAGGDKNRLSPRSLTPTGDPANASPKPLDLKQLKORAAAIPIQV 978
Db 284 -----PKGZPGS-----290

QY	979	TKVHEPR	EDAA	PTKAP	PPPP	PPQNL	QPSD	APQ	QSS	PRK	SS	PPAP	DK	EAF	AAE	1038	
Db	291	----	----	----	----	----	----	----	----	----	----	----	----	----	----	318	
QY	1039	AQKLP	GGPP	CCW	TSL	PLP	VP	PRE	VIK	AS	PHAP	DS	AF	S	YAP	PH	
Db	319	----	----	----	----	----	----	----	----	----	----	----	----	----	----	358	
QY	1099	PPTIS	NP	PL	ISS	A	KH	SV	LER	Q	I	A	S	Q	M	S	
Db	359	PPG	----	----	----	----	----	----	----	----	----	----	----	----	----	1157	
QY	1158	PKKL	AF	SG	VY	K	Q	E	OL	SP	R	G	F	----	----	394	
Db	395	PKG	----	----	----	----	----	----	----	----	----	----	----	----	----	433	
QY	1218	PSD	AI	T	R	G	S	I	T	H	G	T	P	A	D	V	
Db	434	PAG	----	----	----	----	----	----	----	----	----	----	----	----	----	1273	
QY	1274	KGH	V	L	S	E	G	M	----	----	----	----	----	----	----	1328	
Db	471	AG	----	----	----	----	----	----	----	----	----	----	----	----	----	519	
QY	1329	GLM	G	R	A	I	P	P	----	----	----	----	----	----	----	1387	
Db	520	GLP	G	P	A	G	P	E	A	K	P	E	----	----	----	567	
QY	1388	PPS	R	L	T	E	A	Y	T	O	A	L	G	L	K	----	1445
Db	568	GPA	----	----	----	----	----	----	----	----	----	----	----	----	----	594	
QY	1446	LKE	G	S	I	T	O	G	T	P	----	----	----	----	----	1488	
Db	595	----	----	----	----	----	----	----	----	----	----	----	----	----	----	649	
QY	1489	PLD	V	M	A	D	A	R	A	L	E	R	A	C	E	----	1548
Db	650	PAG	A	P	A	P	A	P	A	P	A	P	A	P	A	P	692
QY	1549	PF	A	C	H	L	P	R	G	S	P	V	T	M	R	E	1608
Db	693	PG	A	D	----	----	----	----	----	----	----	----	----	----	----	729	
QY	1609	----	----	----	----	----	----	----	----	----	----	----	----	----	----	1664	
Db	730	G	N	V	G	A	P	A	K	A	G	S	A	G	P	768	
QY	1665	Y	P	P	L	R	G	P	D	T	A	E	N	R	Q	----	1713
Db	769	G	P	P	----	----	----	----	----	----	----	----	----	----	----	812	
QY	1714	S	P	R	E	S	S	I	A	L	N	Y	A	A	G	P	1771
Db	813	P	G	A	D	P	A	G	A	P	A	G	P	A	G	P	867
QY	1772	H	S	S	P	L	S	P	G	T	H	L	T	K	P	T	1831
Db	868	G	E	R	G	P	P	G	M	P	P	G	L	A	G	P	896
QY	1832	E	Q	S	S	G	S	S	G	S	G	G	----	----	----	1886	
Db	897	E	G	S	F	G	R	D	G	S	P	A	K	D	R	941	
QY	1887	I	T	A	V	E	S	K	P	T	V	L	R	S	T	S	1946
Db	942	R	G	E	T	G	P	A	G	P	----	----	----	----	----	963	
QY	1947	R	P	E	R	P	R	A	D	T	G	H	----	----	----	1991	
Db	964	G	P	O	G	P	R	G	D	K	E	T	G	E	Q	1013	
QY	1992	A	T	I	A	R	T	A	K	N	L	A	P	H	A	S	2051


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; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: COLLAGEN ALPHA 1 (I)
; US-09-570-573-18

Query Match      2.7%; Score 351; DB 4; Length 1341;
Best Local Similarity 20.1%; Pred. No. 7.7e-12;
Matches 350; Conservative 106; Mismatches 573; Indels 714; Gaps 81;

QY 722 EALHAGNEVPRGECGATVNNSSDTEISPSHTEAAK-DTGONGPKPPA-TLGADGPP 779
DB 77 EYKNCFAEVPGECC-PVCPDGESEPTQETTGVGPKGDTGPRGPGAPGRGDIP 135
QY 780 -----PGPTTPRRTSRAPTEPTASEATCAPTPP-----PA 811
DB 136 GQGLPGPPGPP-----GPPGPGGNGFNAPQLYGYDEKSTGGISVFG 178
QY 812 PPSAPSAP-----PPVVPKEKEBEETAAAPVEEGE-----EQKPPAAELAVDTGKA 958
DB 179 PMGPSGRGLPGPPGAPGPGZGFZ-----GPPGZPGZPGASGPMGPRGPPGPKGBBGA 234
QY 859 EBPVKSECTEEAEAGPAKGDAAEATAEGALKAEEKGGSGRATTAKSSGAPQDSGS 918
DB 235 GKPR-----PGZRGPPGZGARGLPCTA--GLPGMKHGRGSLGKAGBAGPAG-----283
QY 919 ATCSADEVDEAEGGDKNRLLSPRSLTTPGDPANASPKPLDLKQLKQRAAAIPIQV 978
DB 284 -----PKGZPGS-----290
QY 979 TKVHEPRDAAPTKPAAPAPPQNLQEPESAPQPGSSPRGKSRSPAPPADKEFAAE 1038
DB 291 -----PGZGAPGZMGP-----GPKNSGEPGAPGSK-----318
QY 1039 AQKLPDPCWTSGLPFPPPREVIKASPHADPSAFSAPPCHPLPLGLHDTAREVLR 1098
DB 319 -----GD--TGAKGEPGPGVQ-----GPPGAGEGKRGARGEPTG-----LFG 358
QY 1099 PPTISNPPPLISSAKHPSVLEIQIGAISQMSVOLHVPSYSEHAKAPVGPV-TWGLPLPMD 1157
DB 359 PFG-----ERG-GPGSRG-----PGADGVAGPKGAGERGSGPGAG 394
QY 1158 PKKLAPFGVKQEQLSPRQAGPPESLGVPTQAEASVLRGALGSLVPGSGITGKIPSTRV 1217
DB 395 PKG-----SP-GEARPGAGLPGAKGLTSPGCS-----PGPDGKTGPG-----433
QY 1218 PSDSAITYRGSITHGTPADVLYKGTITRIIGEDSPSLDRGREDLSL-----BKGHVIECK 1273
DB 434 PAGQ-----DGRP-----GPPGPGA-RGQAGVMGFPKGAGEPGK 470
QY 1274 KGHVLSYEGM-----SVTQCKEDGRSSGPPHETAAPKRTYDMMEGRVGRASIASIE 1328
DB 471 AG-----ERGVGPPCAVAGPKDGAGAGQGP-PPAGPAGE-----RGEQGA-GSPGQ 519
QY 1329 GLMGRAPP-ERHSPHLKEQHHRIGSITOGIPRSYVEAQEDYLRREAKLLKRGTPPPP 1387
DB 520 GLPGPAGPPGAGKPG-----QGVPGDLGAPGPGSGARGERFPGERGVQGP 567
QY 1388 PPSRDLTEAYKTQALGPLK-K-PAHEGLVATVKEAGRSIHIEPRELHHTLPLAPRP 1445
DB 568 GPA-----GPRGANGAPNDGAKG-----DAG-----APGAP-----594
QY 1446 LKEGSITQGP-----LKYDTGASTTSGKKHD-----VRSLLGSPGR-----TFP--PVH 1488
DB 595 ---GS---QAPGLQMGPERGAGLPGPKDRGDAGPKGADGSPGKGVRLTGPIGPG 649
QY 1489 PLDVNADALRACYEESLKRPGTPASSGSGSIARGAPVIVPELPGKPRQSPLTYEDHGA 1548
DB 650 PAGAPG-----KGESGSPGAPGTPGARGAPGDRGEPGPP--GPAGFA--GP 692
QY 1549 PFAGHLPRGSPVMTREPTPLQEGSLSSSKASQDRKLTTPREIAKSPHSTVPEHHPHI 1608
DB 693 PGAD-----QOPGAKGEPGDAGKGD-----AGPPGAPGAPGPGPI 729

1609 ----SPYEHLRGGVGVLDLYRSHIPLAFDPTSIPIRGIPIDAAAAYYLPRHLPNPTYPHL 1664
DB 730 GNVGAPGAKGARGAGP-----PGATGFPGAAGRVGP-----PGPS-GNA 768
QY 1665 YPPLYLRGYPDTAALLENROTIINDYITTSOQMHNTATANAQRADML-----RGL 1713
DB 769 GPP-----GPPGAGKEGGKGRGE-----TGAPRGVGEVGPFGPPGAPGEGKS 812
QY 1714 SPRESSALNAAAGPRGIIDLQVPHLPVLVPPT--PGTPATAMDRLAVLPTAPQPFSSR 1771
DB 813 PGADGPAGAPGTPFGQGIAGQGVVCLPGQGERGFPGLPGPSGE-----PGKQGSAGS 867
QY 1772 HSSPLSPGCGTHLTKPTTTSSEERDRDRDREREKSIILTSTTTHHAPIWRPPT 1831
DB 868 GERGPPGPMGPPGLAGPPGESGRE-----CAPGA 896
QY 1832 EGSSGSSGSSGGG-----GSSSRPASHSHAHQHSPISTQDALQORPSVLHNTMKGI 1886
DB 897 EGSPRDSGSGAKGDRGETGPAGPGAGXGAGAPGVGP-----AGKSGD 941
QY 1887 ITAVEPSKPTVLRSTSTSSPVRPAATFPATHCPLGGTLDGVVPTLMEPVLLPKEAPRVA 1946
DB 942 RGETGAPG-----AGVCPGAPGAP-----A 963
QY 1947 RPERPRADTGH-----AFLAKPPARSGLEPASPSKSGSPRPLVPPVSGH 1991
DB 964 GFGPRGDKGETGEOGDRGIKGHRGFSGLQPPGPGSGEOGPGSGASGP-----1013
QY 1992 ATIAITPAKXLAHHASDPDPAPPASADPHREKTSQKFSIQEELRSLGVHSGSYSP 2051
DB 1014 -----AGPRGPGSAGAPGKDLNGLPGPI-----GPPGPRGTG 1048
QY 2052 GVEPVSVSSPSLTHDKGLPKHLELDKSHLEGELRPKOPGVKLGGEAAHPLHLRPLPE 2111
DB 1049 DAGVPGPPGPPG-----PPGPPGPPSAGFDFSLP-----1078
QY 2112 SQFSSPLLTQAPGVKGHQ-----RVVTLAHISEVITQDYTR 2149
DB 1079 -QP-----PQKAKHGGRYRADDANVVRDRDLEVDTLTKLSLQIENIRSPGKX 1128
QY 2150 HHPOQLSAPLAPLAFYSFFGASCPLDLRRPPSDLYLPPDHGAPARGSPHSEGGKSP 2209
DB 1129 KNPAP-----TC--RDLKMCSDW-----KSGEYWDIP 1154
QY 2210 NKTSLVGGGEDGIEPVSPPEGMTPEGHRSASVYVLLYRDGEOTEPSRMG-----SKSPGV 2264
DB 1155 NO-----GCNLDALKVFCNME-----TGETCVTP-----TOPSVAQKNWYISKPKD 1196
QY 2265 TSQPPAFFSKLTES-----NSAMVSKKKQKINKKLNTHNRNPEYNIS 2307
DB 1197 KDRHVWFGEBSMTDGFQFEYGGGSDPADVAIQITFLRLMSTEASQNIYTHCKNSVAYMDQ 1256
QY 2308 QPG 2310
DB 1257 QTG 1259

RESULT 53
US-09-548-608-18
; Sequence 18, Application US/09548608
; Patent No. 6355442
; GENERAL INFORMATION:
; APPLICANT: Oviat, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
```

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
US-09-548-608-18

Query Match 2.7%; Score 351; DB 4; Length 1341;
Best Local Similarity 20.1%; Pred. No. 7.7e-12;
Matches 350; Conservative 106; Mismatches 573; Indels 714; Gaps 81;

QY 722 EALHAGNVPFGESGPAATVNSSTESIPSPHTEAAK-DTGQNGPKPPA-TLQADGPP 779
DB 77 ETKNCGAIVPGECC-FVCPDGSEPTDOETTVGEGPKGDTGPRGPRGPPGPRGDGIP 135
QY 780 -----PGPTTPRRTRSRAPTEPTPASEATGATPP-----PA 811
DB 136 GQGLPGPPGP-----GPPGPGLCGNFAPQLYGYDEKSTGISVPG 178
QY 812 PPSAP-----PPVVKKEEETAAAPVBE-----EQKPPAAELAVDTGKA 858
DB 179 PMGPGPRGLPGPPGAPGZGZ-----GPPGZPGZPGASGPMGPPGPKGBBGZA 234
QY 859 EBPVKSECTEEAEAGPAKDAEAEATAGALKAEKGGSGRATTAKSSAPQDS 918
DB 235 GXPGR-----PGZRGPPGZGARGLPFTA--GLPGMKHGRGFGSLGAKGBAGPAG----- 283
QY 919 ATCSADENDEAGGDKNRLSPRLTPTGPPRANASPKPLDLKQLKQRAAAIPIQV 978
DB 284 -----PKGZPGS----- 290
QY 979 TKVHEPPREDAAPTKAPAPPQNLPQESDAPQPGSSPRGKSRPAPPADKFAFAE 1038
DB 291 -----PGZGAPGZGMP-----GPKGNSGEPGAPGSK----- 318
QY 1039 AQKLPDPCWTSGLPFPVPPREVIVKASPHADPSAFVAPPGHPLPLGLHDTARVPLR 1098
DB 319 -----GD--TGAKGPPGVQ-----GPPGAGBEGKRGARGPGPTG-----LPG 358
QY 1099 PPTISNPPPLISSAKHPSVLRIQAGISQGMVQLHVPVSEHAKAPVGFV-TMGLPLPMD 1157
DB 359 PFG-----ERG-GPGSRGF-----PGADGVAGPKGPPAGERSGPGAG 394
QY 1158 PKKLAPFSGVKQEQLSRPGQAGPPESLGVPTAQEASVLRGTALGSLVPGGSIITKGIPTSTRV 1217

DB 395 PKG-----SP-GEAGRPEAGLPGAKGLTSPGS-----PGDGTGTPPG--- 433
QY 1218 PSDSAITVRSITHTGTPADVLKGTITRIIGEDSPSLDRDREDSL-----PKGHVITYEK 1273
DB 434 PAQ-----DGRP-----GPPGPPGA-RGQAGVMGFPKGGAAGEPK 470
QY 1274 KGHVLSYEGM-----SVTQCSKEDGRSSGPPHETAAKRTYDMMEGRVGRGAISSASIE 1328
DB 471 AG-----ERGVPGPAGVPGAGKGEAGAGQGP-PPAGPAGE-----RGQGPA-GSPGQ 519
QY 1329 GLMRAIPP-ERHSPHLLKEQHIRGSIQTQIPRSVYEAQEDYLRRKXLLKREGTPPP 1387
DB 520 GLPGPAGPEAGKPE-----QGVPGDLGAPGSGARGCFPGERGVOGPP 567
QY 1388 PPSRLTEAYTQALGPLK--PAHEGLVATVKEAGRSIHIPREELNHTPELAPRP 1445
DB 568 GPA-----GPRGANGPNDGAKG--DAG-----APGAP-- 594
QY 1446 LKEGSITQCTP-----LKYDTGASTTGSKKHD-----VRSLIGSPGR-----TFP--PVH 1488
DB 595 ---GS--QCAPGLQMPGERGAAGLPGPKGDRGDAGPKGADGSPKDGVRGLTGIGIPG 649
QY 1489 PLDVNADARALERACYEESLSKSRPGTASSSGSIARGAPVIVPELGKPRQSPLTYEDHGA 1548
DB 650 PAGAPGD-----KGESGSPGAGTGAAGAPDRGEPP--PAGFA--GP 692
QY 1549 PPAGHLPRGSPVTREPTPRIOEGSLSSKASQDRKLTSTPREIAKSHSTVPEHHPHI 1608
DB 693 PGAD-----GQPGAKGEPGDGAKGD-----AGPPGAPGAPGPPGI 729
QY 1609 ---SPYEHLRLRGVSDLYRSHIPLAFDPTSIPIGIPLDAAAAYVLRHLAPNTYPHL 1664
DB 730 GNVGAPGAKGASGAP-----PGATGPPGAGRVGP-----PGPS-GNA 768
QY 1665 YPPLYIRGYPDTAALLENRQTIINDYITSQOMHNTATAMAQADM-----RGL 1713
DB 769 GFP-----GPPGAGKEGKGPRGE-----TGPRGPRGVEGPPGPPGAGEKS 812
QY 1714 SPRESSLAINTAAGRGIIDLSQVPHLPVLPPT--PGTATMDRLAYLPTAPOFFSR 1771
DB 813 PGADGAPAGPTGPGQIAGQGVVGLFGQGERGFFGLPGPSG-----PKQGPSGAS 867
QY 1772 HSSSPLSPGPHLTKPTTTSSRERDRDRDREREKSIILTTTVEHAPIWRPT 1831
DB 868 GERGPPGMPGPPGLAGPPGESGRE-----GAPGA 896
QY 1832 FOSGSSGSSGGG-----GSSSRPASHAHQHSPISPRTQDALQORPSVLHNTMKGI 1886
DB 897 EGSPGRDGSAGAKGDRGETGAPGPGAXGAXGAPGVGP-----AGKSGD 941
QY 1887 ITAVEPSKPTVLRSTSTSSPVRPATFPATHCPGLGGLTGDVYPTLMEPVLLPKEAPRA 1946
DB 942 RGETGAPG-----AGPVGPAGARG-----A 963
QY 1947 RPERPRADTGH-----AFLAKPPARSGLPEASSPSKSGSEPRPLVPVSGH 1991
DB 964 GPOGRGDKGETGEQDRGIKGRGFSGLQFPFGPPGSGGSGASGP----- 1013
QY 1992 ATIARTPAKNIAPHIASPPDPAPPASADPHREKTQSKPFSIQELESLGVLHGSSYSP 2051
DB 1014 -----AGRGPFGSAGAPKDGGLGGLPGPI-----GPPGPRGRTG 1048
QY 2052 GVEPVSVPSSPLTHDKGLPKHLELDKSHLEGLRKPQGPVKLGGAHLPHLRPLPE 2111
DB 1049 DAGVPPGPPG-----PPGPPPPSAGDFSLP----- 1078
QY 2112 SQPSSPLLOTAPGVKHQ-----RVVTLAQHISEVITQDYTR 2149
DB 1079 -QP-----PQEKAKHGGRYVADDANNVRDRLDVEDTTLKSLSQIENIRSPGXR 1128
QY 2150 HHPQOLSAPLAPLYSPFGASCPLDLRPPSDLYLPPDHGAPARGSPHSEGGKRSPEP 2209

Db 1129 KNPAP-----TC--RDLKCHSDW-----KSGEYWDIP 1154
QY 2210 NKTSLVGGGEGDIEPVPPPEGTEPHGSRSAVYPLLYRDGEOTEPGRMG-----SKSPGN 2264
Db 1155 NQ-----GCNLDALKVFCNM-----TGTCVYP-----TOPSVAQKNWYISKPKD 1196
QY 2265 TSQPPAFFSKLTES-----NSAMVSKKQEFINKLNTNHRNEPYNIS 2307
Db 1197 KORHWNFGESMTDGFQFEGGOGSDPADVAIQITFLRLMSTASONITYHCKNSVAYMDQ 1256
QY 2308 QPG 2310
Db 1257 QTG 1259

RESULT 54

US-07-741-940-7

; Sequence 7, Application US/07741940

; Patent No. 5352775

; GENERAL INFORMATION:

; APPLICANT: ALBERTSEN, HANS

; APPLICANT: ANAND, RAKESH

; APPLICANT: CARLSON, MARY

; APPLICANT: GRODEN, JOANNA

; APPLICANT: HEDGE, PHILIP J.

; APPLICANT: JOSLYN, GEOFF

; APPLICANT: KINZLER, KENNETH

; APPLICANT: MARKHAM, ALEXANDER F.

; APPLICANT: NAKAMURA, YUSUKE

; APPLICANT: THLIVERIS, ANDREW

; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Banner, Birch, McKie & Beckett

; STREET: 1001 G Street, NW

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20001-4598

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/741,940

; FILING DATE: 19920109

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Kagan, Sarah A.

; REGISTRATION NUMBER: 32,141

; REFERENCE/DOCKET NUMBER: 1107.035574

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-508-9100

; TELEFAX: 202-508-9299

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2842 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; IMMEDIATE SOURCE:

; CLONE: APC

US-07-741-940-7

Query Match

Best Local Similarity 2.7%; Score 350.5; DB 1; Length 2842;

Matches 473; Conservative 357; Mismatches 1007; Indels 821; Gaps 109;


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Db 2213 -----KQLQANMPSISRG-----RTMHIHPGV-----2235
QY 1764 APOFSSRSSPLSPGCGTHLTATTTSSSERDRDRDRERREKSILTTT---1820
Db 2236 ----RNSSSSTSPVSKGPP-LKTPASKPSEQ-----TATTSPRG 2272
QY 1821 -----VEHAPIWRPTEGSSGSSGGGGSSRPASHAHQSPISPTQDALQOR 1874
Db 2273 AKPSVKSELSPVARQ-TSQIGSSKAPSRGSRDSTPSRPAQPLSRPIQSPGRNSI---2328
QY 1875 PSVLNHTGKGIITAVEPSKPTVLRSTSTSSPVPAATPPATHCPGLGTLDGVY---1930
Db 2329 -----SPGRNGI---SPPNKLSQLPRTSPSTA-----STKSSGSKMSTSPGRQM 2372
QY 1931 ----TLMEPVLLKPEARVPERPRADTGHAFKAPPARSGLEP-----ASSPSKSGSE 1980
Db 2373 SQNLTKOTGLSKVSSI-----PRSESASKGLQNMNGANGANKVLESRMSTKSSGSE 2427
QY 1981 ----PRPLVPVVSGHATIIARTPA-KNLAPHASDPDPAPPASADPHREKTOSKPFIOE 2035
Db 2428 SDRSERPVLVRQSTFTKEAPSPTRLRKLEESASFESLSPPSRPASPTRSQOAT-PVLSPS 2486
QY 2036 LELRSILGYHGSVSPGVPVSPVSSPLTHDKGLPKHLEELDKSHLEGELRPQGPVK 2095
Db 2487 LPDMSLSTH-SSVQAGGWKRLPNLSPTIEYNDGRPAKRDHARSSESFSRL-----PIN 2541
QY 2096 LGG--EAAHLPLRLPESOPSSPLLQAPGVKGHQRVVTLAQHISEVITODYTRHPQ 2153
Db 2542 RSTWTKREHSKH-----SSSLPRVSTWRTGSSSSILSASSESEKAKSEDEKH---2590
QY 2154 QLSAPLAPLYSPFGASCPLDLRRPPSDLYLPPDPHGAARGSPHSEGGKSPENKTS 2213
Db 2591 -----VNSISGTHK-----QSKENQVSAKGTWKIKENEFSPNTSTS 2626
QY 2214 --VLGGEGDIE-----PVSPEGTEPHGRSAVYPLLYRDGEQTEPSRWGSKSPGNT 2265
Db 2627 QTVSSGATNGAESKTIYQMAPAVSKTEDVWVRIEDCPI-----NNRSGRSPTGNT 2678
QY 2266 SOPPAFFSKLTESNAWKSKEIKNLNTHRNPEVNIQPGTEIFNMPAITGTGLM 2325
Db 2679 --PP-----VIUSVEKANPNIKDKDNOAKQNV-----NGSV 2710
QY 2326 TYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEEESPPLSANAPNPLNAGASLPAAMPITA 2385
Db 2711 PMRTVGLNRLNSFIQVADPDQGTKEIKQONNPVPVSETN-----ESSIVERTPFSS 2763
QY 2386 ADGRSDHTLITSPGGGKAKVSG---RPSRKAKSPAPGLASGRDPPSVSVHSEGCNRR 2442
Db 2764 SSS-SKH--SSPSGTVAARVTPFNPNPSPRKSAD-----STSRPQOIP-----2805
QY 2443 TPLTNRVWEDRPSSAGST 2460
Db 2806 TPVNNNT-KKRDSTDTST 2822

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RESULT 56

US-08-452-654-7

Sequence 7, Application US/08452654

Patent No. 5691454

GENERAL INFORMATION:

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; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 94

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,654
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/741,940
; FILING DATE: 08-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.035574
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2842 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: APC
; US-08-452-654-7

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Query Match 2.7%; Score 350.5; DB 1; Length 2842;

Best Local Similarity 17.8%; Pred. No. 2.1e-11; Mismatches 1007; Indels 821; Gaps 109;

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QY 50 ASHLSPGSIQIP--ORRRPSSLSEFO-----PGNERSQELHRLPESHY 91
Db 739 ANIMPGSLPSLHYRKQKALELDAQLSETFDNIDNLSPKASHRSQRHKQSLYGY 798
QY 92 LPELKGSEMEFTESKRPRLELLPDLPLRSPPLATGQAGSBDLT---KDRSL-----141
Db 799 VFDTRHDDNRSDNFTGNMTVLSPYLNTTVLPSSSSSGSLDSSRSEKDRSLERERGIG 858
QY 142 TGKLEPVPSPPHPTDPELELVPPLRSKEELIONMDRVDREITWVEQQLSKLKKQOOLE 201
Db 859 LGNYHPATEN-----PGTSSKRGL-----QISTTAAQIAKV-----ME 891
QY 202 EBAAKPPEPEKVPSPPIESKHSRLVQIITYDENR--KKAEEAHRILEGLGPQVELPLYNQ 259
Db 892 EVSAHTSQEDRSSGSTTE-----LHCVTDERNALRRSSAAH-----THSNTYN- 935
QY 260 PSDTRYHENIKINQAMRKLLIYFKRRNHARKQWKQFCQRYDQIMEALEKKVERIENN 319
Db 936 --FTKSENSNRTCSPYAK--LEYKRSSN-----DSL-----NSVSSDGY 972
QY 320 PRRAKESKVREYVEK-----QFP--EIRKQRELQERMSRVGQSGSLMSAARSE 369
Db 973 GKRQMKPSESIESDEDESKFCYGOYPADLAHKIHSANHMDNDGELDTPINYSKYSD 1032
QY 370 HEVSEIIDGLSEQENLEKQMRQLAVIPPMYDADQORIKFINMGLMADPMKVKYDQVM 429
Db 1033 -----EQLNSGRQ-----SPQNERWARPKHIEDEIKQSEQRQSR 1068
QY 430 NMWSEOE--KETFRKFMQHPKNFGLIASFLERKTVACVLYYLTQKNYKSLVRRSY 487

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Db 1069 NQSTTPVYTESTDDKHLKEQPHFG-----QOECVSPYRSGANGSETNRVGSNH 1118
Qy 488 RRRGSKQQQQQQQQQQQQQQQQMPRSSQEEKDEKEKE-----AEKEEKPEVEND 541
Db 1119 --GINQVQSLSQEDDYEDDPTNYRYERYSEEEQHEEBEERTNYYSIKYNEEKRHVDQ 1175
Qy 542 KEDLLKEKTP-----DTSGEDN-DEKEAVASGRKTANSQGRKRIRITRMA 587
Db 1176 IDYSLKYATDIPSSOKQSFSSQSSQSKTHMSSSENTSTPSSNAKRONQLHPSSA 1235
Qy 588 NEANSEBAITPOQSAELASMELNESSRWTEEMETAKKLGLEHGNWSAIAARMVGSKTVS 647
Db 1236 QSRSGQ-----PQAAATCKVSSINQETIQTVCVEDTP-----ICFSRCSLSUSS 1280
Qy 648 QCNFYFNKKRQNLDD--EILQOKLKMKEK--ERNARRKKKKAPAAASEEAAFPVVEDE 703
Db 1281 SAEDEIGCNOTQOADSANTLQIAEIK-EKIGTRSAEDPVSEVPAVSQH-----PRTKSS 1334
Qy 704 EMEASGVSGNEE-----EMVEEAEALHASGNEVPRGE-----CSGPATVNSSDTSIPS 753
Db 1335 RLOGSSLSSESARHKAVEFSSGAKSPSKGAQTPKSPPEHYVQETPLMFSCRCTSVSLSLS 1394
Qy 754 PHTAAKOTGQPKPATIGADCP-----PGPPTPRETSRAPIEPTPASEATGAPT 808
Db 1395 FESRSIASSVQSEPCSGMVGSIISPLDPSPGQTMPPSRSK-----TP 1438
Qy 809 PPAPPPSADPPVVPKEEKEETAAAPVBEGBEQPPAAEELAVDTGKA---EEPVKSE 865
Db 1439 PP-PPQTAQTKREVPKK-----APTAERESGPKQAAVNAVQVQLPADILLHF 1490
Qy 866 CTEEAEEG-----PAKGKDAFAAEATAEGALKAKEKGGSGRATTA---KSSGAPQDS 915
Db 1491 ATESTPDGFCSSLSALSLEPPIQKDELIMPPVQENDNGNETESEQPKESNENQEK 1550
Qy 916 DSSATCSA--DEVDEABGGP-----KNLLSPRSLLTPTGDPANASPOKPLDLKQLKOR 969
Db 1551 EAEKTIIDSEKDLDDDDIEILEECIISAMPT-----KSSRAKKP-----AQT 1596
Qy 970 AAAIPPIQTVKHEPPREDAAPTKAPAPPONLQEPESDAPQOQSS--PRGKRSRPAP 1028
Db 1597 ASKLPVPVARKPQLPVYKLLPSQ-----NRLQPKHVSFTFGDDMPR----- 1639
Qy 1029 PADKEAPAAQKLPGLPDPGCPWTSGLPFPVPREVIKASHAPDPSAFSPAGHPPLGL 1088
Db 1640 -----VYCVGEG-----TPINPSTA-----TSL 1656
Qy 1089 HDTPARPVLPPTTISNPPPLISSAKHPSVLERQIGAISQGMVOLHVPYSEHAKAPGVV 1148
Db 1657 SDL-----TIESPP-----NELAAGEVVRGGAQSGEFKERTIPT 1691
Qy 1149 TMGLPLPMDPKLAPFSGVQEOQLSPRQAGPPESLGV-----TAQEAASVLRGTALGV 1203
Db 1692 -----EGSTDEAQGGKTSSTVITPELDDNKAEGDILAEINSAM 1731
Qy 1204 PGG-----SITKGIPTSTRVPSDAITYR-----GSITHGTPADVLVYKGTITRI 1246
Db 1732 PKGSKHPFRVKKIMDQVQASASSAPKNQLDGKKKTPSPVKPIPQNTVEYTRVRK- 1790
Qy 1247 IGEDSPRLDRGREDSLPKGHVIEYEGKGVLSYEGGMSVTCQSKED---GRSSGGPHE 1303
Db 1791 -NADSKNNLNAERVFSDNK-----DSKKQNLKNSKDFDKLPNNEDVRVGSFAFDSPHH 1844
Qy 1304 TAAPKRTYDMGREGVRGAISSASTEGL-----MGRAIIPPRHSPHLEKQHHIRGSI 1355
Db 1845 -----YTIETGTPYCFSRNDSLSLDFDDDDVLSR-----EKAELRKAKENKESAKV 1893
Qy 1356 TOGIPRYSYBAQEDYLREAKLLKREGTPPP-----PPPSRDL-----TEAYKTQ 1400
Db 1894 TSHTELTSNOOSANKTOAIAKQPINRGPKPILOKQSTFFQSSKDIIPDRGAATDEKLQNF 1953
Qy 1401 ALGPKLKPAGHGLVATVKAGRSIHEIPRELRHT-----PELPLAPRPLEKGSIT 1452
Db 1954 AIENTPVCFSHNSLSLSLSDIDQENNNKENEPKETEPDPSQGEPSKQASGVAPKSFHV 2013

Qy 1453 QGTPLKYDTCASTGT-----SKKHVRSLSIGSPGR 1482
Db 2014 EDTPVCFSRNSLSLSIDSEDDLQECISSAMPKKKPSRLKGDNEKHSPRNMGGLIGE 2073
Qy 1483 TFPVPHPLVMDARALERACYEESLSKSRPCTASSSGSSTARCAPVIVPELGRKQRSPLT 1542
Db 2074 -----DLTLDKDOIQRDPSEHGLS--PDSEFDMKAIQEGANSIVLSL----- 2114
Qy 1543 YEDHGAPFAGHLPR-----GSPVTMRPTPRLQEGSLSSSKASQDRK 1584
Db 2115 ---HQAARACLQRQASSDSDLSLSKSGISLSPHIL-----TPDQEKPTNSKG----- 2163
Qy 1585 LTSTPREIAKSPHSTVEHHHPHPISPYEHLLRGV-SGVDLYRSHIPLAFDPTSLPRIGPL 1643
Db 2164 ---PRILKPGEKSTL-----ETKKIESKGIKGGKVKYS----- 2196
Qy 1644 DAAAAVYLPHRLAPNTYPHYLPYLIIRGVYDPTAALENQTIINDYITTSQOHHNTATAM 1703
Db 2197 -----LITG-----KVRNSEISGM----- 2212
Qy 1704 AQRADMLRGLSPRESSLALNYAAGPRGIIDLQVPHLPVLVPTPGTGPATAMDRLAYLPT 1763
Db 2213 -----KQPLQANMPSISRG-----RTWIIHIGV----- 2235
Qy 1764 AQOFFSSRHSSPLSPGPTHLTPTTSSSERDRDRDRDREREKSIILTTT----- 1820
Db 2236 ---RNSSTSTSPVSKGPP-LKTPASKSPSEGO-----TATTSPRG 2272
Qy 1821 ---VEHAIWPRQTEQSSSGSSGGGGSSRPASHSHAHQHSPIPRQDQALQOR 1874
Db 2273 AKPSVKSELSPVARQ-TSQIGSSKAPSRGSDSTPSRPAQOQLPSRPIQSPGRNSI--- 2328
Qy 1875 PSVLHNTGMKGIITAVEPSKPTVLRSTSTSSVPVPAATFPFATHCPLGGTLDGVVP--- 1930
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Qy 1931 ---TLMPEVLLPKPEAPRPARPERPRADTGHAFILAKPARSGLEP-----ASSPSKSGSE 1980
Db 2373 SQQLTKQTGLSKVASSI-----PRSESASKGLNQMNGANGKANKVELSRMSTSKSGSE 2427
Qy 1981 ---PRPLVPPVSGHATIAITPA-KNLA PHASFPDPAPPASADPHREKTQSKPFSIOE 2035
Db 2428 SDRSERPVLVRQSTFIKEAPSTLRRKLEESASFESLSPSRSPASPTRSQAT-PVLSPS 2486
Qy 2036 LEURSLGYHGSYSPEGVEPVSPVSPSLTHDKGLPKHLEELDKSHLEGELRPKQPGPVK 2095
Db 2487 LPDMSLSTH-SSVQAGGWKLPNLSPPTIYNDGRPAKRHDIAARSHSESFSL-----PIN 2541
Qy 2096 LGG--BAAHLPHLRPLPESQPSSSPLLQTAGVYKHQHVVTLAQHISEVITQDYTRHPQ 2153
Db 2542 RSGTWKREHSHK-----SSSLPRVSTWRTTSGSSSSILSASSESEKAKSEDEKH--- 2590
Qy 2154 QLSAPLPAPLPSYPGASCPLVLRPPSDLYLPPDHGAPARGSPHSEGGKRPPEPNKTS 2213
Db 2591 -----VNSISGTK-----QSKENQVSAKGTWIRKIKENEFSPNTSTS 2626
Qy 2214 --VLGGEGEGIE-----PVSPEEGMTEPGCHSRSAVVPLLYRDGEQTEPPSRMGSKSPGNT 2265
Db 2627 QTVSSGATNGAESKTLIYONAPAVSKTEDVWVRIEDCPI-----NNPRSGRSPGNT 2678
Qy 2266 SQPPAPFSLKTESNANVKSKEQINKKLNTNHRNEPEVYNISQFTGTFBNMPTAITGTGLM 2325
Db 2679 --PP-----VIDSVSEKANPNIKDSKDNQAKQNV-----GNGSV 2710
Qy 2326 TYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEESEPLSANAFNPLNASLSLPAAMPITA 2385
Db 2711 PMRTVGLNRLNGFIQVDAPDQGTETIKPGQNNPVPVSETN-----ESSIVERTPFSS 2763
Qy 2386 ADGRSDHTLTSQGGGKAKVSG---RPSRFAKSPAPGLASGDRPPSVSVHSEGDGNNR 2442
Db 2764 SSS-SKH---SSPSGTVAAVRTVPPNPNPSPRKSAD-----STSRPSQIP----- 2805

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1692 -----EGRSTDBAOGKTSSTVITPELDDNKAEEGDILAECSAM 1731
1204 PGG-----SITKGIPISTRVPSDAIYR-----GSTHTGTPADVLYKGTITRI 1246
1732 PKGSHKPFVKKIMQVOQASASSAPNKNQDGGKKKTSVPKPIQONTYRTRVK- 1790
1247 IGDSPSLDRGREDLSPKGVHIVEGKKGHLVGEVGMSTVQCSKED---GRSSSGPPHE 1303
1791 -NADSKNNLNAERVSFNK-----DSKKQNLKNNKDFNDKLPNEDRVGSGFAPSPHH 1844
1304 TAAPKRTYDMGVRGVRGAISSASIEGL-----MGRAPIPRHHGPHLKEQHHRGSI 1355
1845 -----YPIEGTPTCFSRNDSLSLDDFDDDDVLSR-----EKAELRKAKENKESEAKV 1893
1356 TQGIPIRSYVEAQEDYLREAKLLKREGTPP-----PPSRDL-----TEAYKTQ 1400
1894 TSHTELTSNOOSANKTOAIKQPINRGQPKPILOKQSTFPQSSKDIPIRGAATDEKLQNF 1953
1401 ALGPKLKPAGELVATVKEAGRSIHEI PREELRHT-----PELPLAPRPLKESGIT 1452
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1453 QGTPLKYDTGASTTG-----SKKHVRSLLIGSPGR 1482
2014 EDTPVCFSRNSSLSSLSLSDIDQECISSAMPKKKPSRLKGDNEKHSPRNMGGLGE 2073
1483 TFPVPHPLDMADARALERACYESLKSRRPGTASSGGSIARGAPVIVPELGPROSPLT 1542
2074 -----DLTLDLKDIOIRPDSEHGLS--PDSENFOWKAIOEANGSIVSSL----- 2114
1543 YEDHGAPFAGHLPR-----GSPVTMREPTRLQEGSLSSSKASQDRK 1584
2115 ---HQAAAACTQRASSDSLSLSKSLGSLSPFHL---TPQBEKPTSNKG----- 2163
1585 LTSTPREIAKSPHSTVPEHHPIPSVPEHLLRGV--SGVDLYRSHIPLAFDPTSIPRGIPL 1643
2164 ---PRILKPEKSTL-----ETKKIESKGIKGGKVKYS----- 2196
1644 DAAAAAYLPHLAPNPTYPHLYRGPVDTAALNRQTIINDVITSQOMHHNTATAM 1703
2197 -----LITG-----KVRNSNSISGOM----- 2212
1704 AQADMRLGSLPRESSIALNYAAGPGI IDLSQVPHLPVLVPTPGTPTAMDRLAYLPT 1763
2213 -----KQPLQANPISRG-----RTMIHPIGV----- 2235
1764 APQFSSRHSSPLSPGGTHLTKPTTSSSRERDRDRDREREKSLTSTTT--- 1820
2236 ---RNSSSSTSPVSKKGP--LKTTPASKSPSEQ-----TATTSPRG 2272
1821 -----VEHAPIWRPTEQSGSGSGSGSGSGSRPASHAHQHPISPRQDALQOR 1874
2273 AKPSVKSLSVPAQ--TSQIGSSKAPSRGSRDSTPSRPAQQLSRPIQSPGRNSI--- 2328
1875 PSVLHNTGMKGIITAVEPSKPTVLRSTSTSPVRPAATFPFATHCPGLGTLGTVYP--- 1930
2329 -----SPGRNGI---GPPNKLSQLPTSSPSTA-----STKSGSGKMSVTSFGQM 2372
1931 ---TLMEPVLLPKEAPRVARPERPADTGHAFKAPARSGLP-----ASSPSKSGE 1980
2373 SQONLTKQTLKQNASI-----PRESASKGLNQMNNGANKVLSRMSSTKSGSE 2427
1981 ---PRPLVPVPSGHATIAITPA--KNLAPHASDPDPAPPASADPHREKTQSKPFSIQE 2035
2428 SDRSERPVLVRQFTTKEAPSTLRRKLEESASFESLSPSRPASPTRSQAQI--PVLSPS 2486
2036 LEURSLGYHSGSVSPGEVPSVPSPLTHDKGLPKHLELDKSHLEGLRKPQGPVK 2095
2487 LPDMSLSTH--SSVOAGWRKLPNLSPTIEYNDGRPAKRHDIARSHSESPSL-----PIN 2541

2096 LGG--FAAHLPHLRPLPESQSPSSPILQOTAPGVKGHQRVVTLAQHISEVITQDYTRHHQ 2153
2542 RSGTWKREHSHK-----SSSLPRVSTWRTGSSSSILSASSESEKAKSEDEKH--- 2590
2154 QLSAPLPAPLYSPPGASCPLDLRRPPSDLYLPPDPHGAARGSPHSEGGKRPENPKTS 2213
2591 -----VNSISGTYK-----OSKENQVSAKGTWRIKIKENEFSPNTSTS 2626
2214 --VLGGEGDIE-----PVSPPEGMTEPHGHSASVPLLYRDGEQTEPSRMGSKSPGNT 2265
2627 QTVSSGATNGAESKTLIYQMAPAVSKTDVWVIEDCPI-----NNPRSGRSPGTNT 2678
2266 SOPPAFFSKLTESNAMYKSKQEIKNKLNTHNRPEVYNISOPGTEIFNMPAITGTGLM 2325
2679 --PP-----VIDSVSEKANPNIKDSKNOAKQNV-----GNGSV 2710
2326 TVRSQAOVEHASTNMGLEAIIRKALMGKYDOWEESPPLSANAFNPLNASASLPAAMPITA 2385
2711 PMRTVGLNRLNSFIQVADPDQKGTIKPGQNNPVPVSETN-----ESSIVERTPFSS 2763
2386 ADGRSDHTLTSPGGGKAKVSG---RPSGRKAKSPAPGLASGDRPPSVSVHSEGDGNNR 2442
2764 SSS-SKH--SSPSGTVAARVTPPNYNSPRKSSAD---STSARPSQIP----- 2805
2443 TPLTNRWEDRPSSAGST 2460
2806 TPVNNNT-KKRDSTKTDST 2822

RESULT 58

US-08-452-655B-2
; Sequence 2, Application US/08452655B
; Patent No. 5783666
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,655B
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,548
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/741,940
; FILING DATE: 08-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.49964

Db 1120 ---G1NQV5QLCQEDDYEDDKPTNYSERYSEBEEQHHEERPTNYSIKYNEEKRHVDOP 1176
QY 542 KEDLLKEKTD-----DTSGEDN-DEKEAVASGRKTANSQGRKRIRTSMA 587
Db 1177 IDYSLKVATDIPSSQKQSFSSKSSQSQSKTHMSSSENTSTPSNAKRONQLHPSSA 1236
QY 588 NEANSEBAITPQSAELASLMELESSRWBTEEMETAKKGLLEHRNWSAJARMVGSKTVS 647
Db 1237 QSRSGQ---PQAAATCKVSSINQETIQTICVEDTP-----ICFSRCSLSLSL 1281
QY 648 QCNFNYNKKRONLD--EILQHKLMKEK--ERNARRKKKAPAAASEBAAPPPVVEDE 703
Db 1282 SADEIGCNOTTQEADSANTLQIAEIK-EKIGTRSAEDPVSEVPAVSQH-----PRTKSS 1335
QY 704 EMEASGVSGNEE---EMVEEAELHASQNEVPRGE-----CSGPAIVNNSDTSIPS 753
Db 1336 RLOQSSLSSESAHKAVEFSSGAKSPSKGAQTPKGPPEHYQETPLMFSTRCTSVSLDS 1395
QY 754 PHTAAKDTQONGPKPPATLGADGP-----PPGPPTPPRTSRAPTEPTPASEATGAPT 808
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QY 866 CTEEAEEG-----PAKGDAEAAEATAEGALKAEKSGSGRATTA---KSSGAPDS 915
Db 1492 ATSTFDGFCSSLSALSLEDEPFIQKDVLELRIMPVQENDNGNETESQPKESNQEOK 1551
QY 916 DSSATCSA--DEYDEAEGGD---KNRLASPRPSLLTPTGDPANASPOKPLDLKQKQOR 969
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Db 1641 ----VYVEG-----TPINFSTA-----TSL 1657
QY 1089 HDTARPVLPRPTTISNPPPLISSAKHPSVLERQIGAISQMSVQLHVPVSEHAKAPGVV 1148
Db 1658 SDL-----TIESPP-----NELAAGEVRGCAQSGSEFEKRTIPT 1692
QY 1149 TMGLPLPMDPKKLAPSGVQBQSLSPRQAGPPESLGVF-----TAQASVLRGTAGLV 1203
Db 1693 -----EGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAEICINSAM 1732
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Db 1792 -NADSKNNLNAERAVFSDNK-----DSKQNLKONSQDFNDKLPNNEDVRGSAFDSPIH 1845
QY 1304 TAAPKTYDMMEGRVCRATSSASIEGL-----MGRAPIPERHSPHLKEQHIRGSI 1355
Db 1846 -----YTPIEGTPVCFGRNDSLSLDFDDDDVLSR-----EKAELRKAKENKSEAKV 1894
QY 1356 TQCIIPSYVEAOEDYLRRBAKLLKREGTPPP-----PPPSRDL-----TEAYKTO 1400
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QY 1401 ALGPLKLPKPAHEGLVATVYKAGRSIHIEPRBELRHT-----PELPIAPRPLKEGSIT 1452
Db 1955 AIENTPVCFSHNSLSLSLSDIOENNNKENEPIKETEPDPSQGEPSKPOASGVAPKSFHV 2014
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Db 2015 EDTPVCFSRNSSLSSLSIDSEDDLQEOCISAMPKXKPSRLKGNERNKPRNMGGILGE 2074

QY 1483 TPPPVPPLVDMADARALERACYEESLSKSRPCTASSSGGSIARGAPVIVIVELGKPROSPLT 1542
Db 2075 -----DLTLDLKDIQRPDSEHGLS--PDSENFDMKAIQEGANSIVSSL-----2115
QY 1543 YEDHGAPPAFHLP-----GSPVTMEPTPRLQEGSLSSSKASQDRK 1584
Db 2116 ---HQAANAACLSRQASSSDSILSKSGISLGGSPHL---TPDQEEKFTSNKG-----2164
QY 1585 LTSTPREIAKSPHSTVPEHHPIPSYEHLLRGV--SGVDLYRSHIPLAFDPTSIPRG1PL 1643
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QY 1644 DAAAAYYLPRHLPAPNPTYPHLYPPYLRGPYDPALENRQTIINDVITSQMHNTATAM 1703
Db 2198 -----LITG-----KVRNSSEISQOM-----2213
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Db 2214 -----KQPLQANMPSISRG-----RTMHIIPGV-----2236
QY 1764 APQFSSRHSSPLSPGGTHLTKTPTTSSRRERDRDRDREREKSIILTSTTT---1820
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QY 1821 -----VEHAPIWRPCTEQSSGSSGSSGSSSPASHSHAHQHSPISPRTQDALQOR 1874
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QY 1875 PSVLNHTMGKIITAVEPSKPTVLARSTSTSSVPVPAATPPPATHCPLGTLGQVVP---1930
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QY 1931 ---TLMEPVLLPKEAPRVARPERPADTGHAFIAPKPARSGLEP-----ASSPSKSGE 1980
Db 2374 SQOQLTKOTGLSKNASSI-----PRSEASKGLNQWNGANGKVKVELSRMSTKSSGSE 2428
QY 1981 ----PRELVPVPSGHATTARTPA-KNLAPHHASPDPAPPASADPHREKTKOSKPSIOE 2035
Db 2429 SRSERPVLVROSTTIKEAPSTLARKLEESASFESLSPSPSPAPSTRSQAT--PVLSPS 2487
QY 2036 LEIRSLGVHSGSYSPGVEPVSPVSPSLTHDKPLPKHLEELDKGHELELRPKQPGVYK 2095
Db 2488 LPDMSLSTH--SSVQAGWKLPPNLSPTIEYNDGRPAKHEDIARSHSESPSL-----PIN 2542
QY 2096 LGG--EAAHLPHLRPLPSQSPSSPLLQTPAGVKGHQVRVTLAQHISEVITQDYTRHHQ 2153
Db 2543 RSGTWKREHSKI-----SSSLPRVSTWRRRTGSSSSSILSASSESEKAKSEDEKH---2591
QY 2154 QLSAPLAPLXPFGPCAPVLDLRRPPSDLYLPPPDHGAPAGSPHSEGGKSPSPNKTS 2213
Db 2592 -----VNSISGTK-----QSKENQVSAKGTWRKIKENEFSTNSTS 2627
QY 2214 --VLGGEDGIB-----PVSPPEGMTEPHGSRSAVYPLLYRDGQTEBPSRMGSKSPGNT 2265
Db 2628 QTVSSGATNGAESKTLIYQMAPAVSKTEDVWVRIEDCPI-----NNPSRGRSPTGNT 2679
QY 2266 SQPPAFFSKLTESNGAMVKSQKQENKLNKLNTHRNEPEYNISQPGTEIFNMPAITGTGLM 2325
Db 2680 --PP-----VIDSVSEKANPNIKOSKNOAQKNV-----GNGSV 2711
QY 2326 TYRQAOVQEHASTNMGLEAIRKALMGKYDOWEESPPLSANAFNPLNASASLPAAMPITA 2385
Db 2712 PNRVTGLENLNSFLQVADAPQKGTETKPGQNNPVPVSETN-----ESSIVERTPSS 2764
QY 2386 ADGRSDHLLTSPGGGKAKVSG---RPSRRKAKSPAGLAGDRPPSVSSVHSEGDENRR 2442
Db 2765 SSS-SKH--SSPSGTVAARVTPFNYPNPSPRKSSAD---STSARPSQIP-----2806
QY 2443 TPLTRVWEDRPSAGST 2460
Db 2807 TPVNNNT-KKRDSKTDST 2823


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; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2843 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; US-08-450-582-7

Query Match      2.7%; Score 350.5; DB 3; Length 2843;
Best Local Similarity 17.8%; Pred. No. 2.1e-11;
Matches 473; Conservative 357; Mismatches 1007; Indels 821; Gaps 109;

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Db 740 ANIMSGSLSLSLHVKQKALEAELDAQLSETFDNIDNLSPKASHRSKQRHKQSLGYD 799
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QY 92 LPELGKSEMEFTIESKPRLELLPDLRLPSPLIATQOPAGSEDLT---KDRSL----- 141
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Db 800 VFTNRHDDNRSDNFNTGNMTVLSPYLNTVLPSSSSRSGSLDSRSSEKDRSLERERGIG 859
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 142 TQKLEVPSPSPHTDELELVPRLSKELIQMDRVREITWVEQOISLKKKKQOOLE 201
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 860 LGNYHPATEN-----PGTSSKRL-----QISTTAAQIAKV-----ME 892
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 202 EEAAKPEPEKPPPIESKHSRLVQIIVDENR--KKAEEAHRILEGLGPQVELPLVNO 259
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Db 893 EVSAIHTSQEDRSSGTT-----LHCVTDERNALRRSSAAH-----THSTYN- 936
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QY 260 PSDTROYHENIKINQAMRKLLILYFKRRNHARKQKFCQRYDQLMEALEKKVERIENN 319
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 320 PRRRAKESKVEYIEK-----QPP-EIRKQRELOEQMRQVRGQSGLSMSARSE 369
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Db 974 GKGQMKPSTIESSEDDSKFCYGOYPADLAHKHSANHMDNDGELDTPIINYSIKYSD 1033
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QY 370 HEVSEIIDGLSEOLEKQMRQLAVIPMLYDADQRIKFINNGLMADPMKVKYDQVM 429
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Db 1034 -----EQUNSGRQ-----SPSQNERWARPKHIIIEIKOSEQRQSR 1069
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 430 NMWSEQ--KETPREKFMQHPKNFGLIASFLERKTVAECLVYLLTKQENYKSLVRSY 487
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1070 NQSTTPVYTESDDKHLKFPQPHFG-----QCECVSPYRSRGANGSETNRVGSNH 1119
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QY 488 RRRGKSQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 541
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1120 ---GINQNVQSILCOBDDYEDDKPTNYSERYSSEEQHEEERPTNYSIKYNEEKRHVDQ 1176
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QY 542 KEDLLAKETD-----DTSGEDN-DEKEAVASKRGTANSQGRKRGRITRSM 587
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Db 1177 IDVSLKVAIDIPSSQKQSFSSKSSGQSKQSKTEHMSSENTTPSSNAKQNLHPSSA 1236
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 588 NEANSEAITPQOASBLASMELESSEWTEETAKGGLLEHGRNWSAIRMVGSKTYS 647
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QY 648 QCNFVNYKQNLND--EILQHKLMKEK--ERNARKKKKAPAAASEEAAPPPVVEDE 703
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1282 SADEIGCNQTOEADSAANTLQIAEIK-EKIGTRSAEDPVSEVPAVSQH-----PRTKSS 1335
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 704 EMEAGVSGNEE-----EMVEEAELHASGNEVPRGE-----CSGPATVNSSDTSIPS 753
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1336 RLQGSLSSESARHKAVEFSSGAKSPSKSAQTPKGPPEHYVQETPLMFSRCTSVSSLDS 1395
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 754 PHTAAKDTQNGPKPPATLGADCP-----PPGPPTPPRTPRAPTEPTPASEATGAPT 808
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1396 FESRSTASSVQSPCGSMVSGIISPSDLPSQQTWPPPSK-----TP 1439
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 809 PPAPPSAPSAPPVVPVPEKEEETAAAPPVEEGEQKPPAAABELAVDTGKA---EFPVKSE 865
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2237 ----RNSSSTSPVKSGPP-LKTPASKSPSEQ-----TATTSPRG 2273
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```


RESULT 65

US-09-854-856-58
; Sequence 58, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 2004
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2004)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-58

Query Match 2.6%; Score 349.5; DB 4; Length 2004;

Best Local Similarity 20.5%; Pred. No. 1.6e-11;

Matches 374; Conservative 187; Mismatches 690; Indels 575; Gaps 81;

QY	822	VPKEEKEETAAAPPVEGEQKPPAAEELAVDTGKAEEVPKSECTEEAEAGKAKGDAE	881
DB	472	VP-EDVAQMVESGYCEGDHKTMAKAKDRVSLIKRKEQROLVREEQK-	521
QY	882	AAEATAEGALKAEKKEGGSG-RAATKAKSAPQDSDSATCSAD-EVDEAGGDKNR	936
DB	522	--KKQESSLKQVEQSSASQGIKQLPSASTGIPASTTSASVSTQVEEPEADQHQ	579
QY	937	LLSPRSL-----LPTGD-----PRANASPKPLDLKOLKORAA-----IPPI--	976
DB	580	LOQQPSISVLSGTVDSGGSSVFTESRVSSQQTVSYSQHEQAHSTGTVPGHIPSTVQ	639
QY	977	--OVTKVHPPREDAAPTKAPAPPPPPONLOPESDAQO-----QPCSSPRGKSRPAPP	1029
DB	640	AOSQPHGVPPSSVQOQIQOTAPPQQTQVYLSQTSSEATTQAQPVSOQAPQVLPQVS	699
QY	1030	ADKEAFAAEAKLPGDPPCWTSGLPFPVPPREVIKASPHADPDSAFSAPPGLPLGLH	1089
DB	700	AGQGP-----PPR-----LPPQYFGDS--NIAPSSNVASVCIH	731
QY	1090	DTARPVL--PRPTISNPPLIISAKHPSV---LERQIGAISQGMVQLHVPYSEHAKAP	1144
DB	732	ST---VLXPPMPTEVLATPGYFTVQPYVESNLLVPMGVG--GGQVQVSQPGGSLAQAP	786
QY	1145	VGPVTWGLPLPMDPKKLAPSGVKQEQLSPRGAQGPESLGV-----PTAEASVLRG	1197
DB	787	TTSSQAV-----LESTQGV-----SQVAPAEPVAVAQOATQPTTLASSV--D	828
QY	1198	TALGSVPGGSITKIGIPSTRVPDSAITYRGSITHGTADVLVYKGTITRIIGEDSPSLDR	1257
DB	829	SAHSDVASG-MSDG--NENVPSSG-----RHEGRTKHYRKSVRSR	870
QY	1258	GREDSLPGKHVIYEGKKGHVLSEYGGMSVTQCSKE-----DGRSSSGPPHET	1304
DB	871	HEKTSRPLRLNVSNKGD-----RVVECCLETHNRKMVTFKFDLDGDN---PEEI	918
QY	1305	AAPKRYDMMGEVRGVAISSASIEGLMGRAPPERHSPHLKQOHIRGSIQIGIPRSYV	1364
DB	919	ATIMVANDFI-----LAIERESFVDQVREII-----EKADEMLSEDVSVEPEGDQGL--ESL	968

QY	1365	EAQEDYLREAKLLKKEGTTPPPPPSRDLTEAYKTOALQGLKLKPAHEGLVATVYKAGRS	1424
DB	969	QKDDYFGSGOKLEGFKQIPASSM-----PQIGIPTSSLTQVHVSAGRR	1016
QY	1425	--IHEIPREELRHTPELPLAPRLKESITQGTPLKYVDTCASTGSK-----KHDVRSL-	1476
DB	1017	FIVSPVESRLRESKVFP-----SEIT-----DTVAASQASPGNLSHSASLS	1061
QY	1477	-----IGSPGRTFPVPHPLDVMDARALERACYEBSLSKSRPG	1513
DB	1062	LQQAPELRLAQMTEGTPNTAPPNFSHTGTFPVVP-----FLSSIAGVPT	1107
QY	1514	TASSSGSIIARGAP-----VIVPELKGPROSL--TYEDHGAPFAGHLPRGSPVTMRE	1564
DB	1108	TAAATAPVPATSSPNDISTSVIQSEVTVPTEBGIAGVATSTGWTSGGL-----	1157
QY	1565	PTPRLOEGSLSSSKASQDRKLSTPREIA-----KSPHSTVPEHHPHPISPVHLLRGVSGV	1621
DB	1158	PIPPVSESPVLSVSSWSS-----ITIPAVSISTTSPSLQVPTSTSEIV-----VSST	1204
QY	1622	DLYRSHIPLAFDPTSIPIRGIPIDAAAAYVLPRLAPNPTVPHLYPPVLI-----	1670
DB	1205	ALYPS-----VTVSATSAGSGSTATGPK-----PFAVSOQAAGSTVVG	1245
QY	1671	-----RGYPDTAALENRQ-----TIINDYITSQOMHNTATAMA-----	1704
DB	1246	ATLTSVSTTTSFPSTASQLSIQLSSSTSTPTLAEVTVVSAHSLDKTSHSSTTGLAFSLA	1305
QY	1705	-----ORADMLRGLSPR-----ESSLALNYAAGPRGIIIDLSQVPHLPVLVPP	1746
DB	1306	PSSSSPFGAGVSSYISQPGGLHPLVIPSVIASTPILPQAAGPTSTPLLPQVPSIPPLVQ	1365
QY	1747	TPCTATAMDRLAYLPTAQPFSRRSSSPLSPGGP--THLTKTPTTSSSRERDRDRERD	1805
DB	1366	VANVPV---QOTLIHSQFQP-----ALLENQPHTHCP-----EVD	1398
QY	1806	RDREREKSILTSTTTVEHAPIWRPGTEQSSGSGSGGGSSSRPASHASHAHQHSPISP	1865
DB	1399	SDTQKAPGIDDIKLTLE-----KLSLFSHSSSGA-----QHASVSL	1437
QY	1866	RTODALQQRPSVLHNTGMKI--ITAVEPSKPTVLRSTSSVPRPAATPPPATHCPILGT	1924
DB	1438	ETS-----LVIESTVTPGIPTTAVAPSK--LLTSTT-----STCLPPTNLPLG--	1478
QY	1925	LDGVYPTLMPEVLLPKEAPRVARPERPRADTGHAFKAPKPARSGLPASSPSKSGSRPL	1984
DB	1479	-----TVALPVTVPVTPGOVSTPVSTTSSGVKPGTAPSKPLTKAP	1519
QY	1985	VPPVSGHATIAITPAKNLAPHASDPDPAPPASADPHREKTQS--KPFSTIQEILELSGY	2043
DB	1520	VLPVGTPELPAGTLPSEQL-----PPFPGPSL-----TQSQQPLEDLDAQLR---	1560
QY	2044	HGSSYSPGVEPVSVSPSLSLTHDKGLPKHLEBDKSHLEGLRKPQPGVKLGGEAAHL	2103
DB	1561	--RTLSPXITVTSV-----GPVSMAPTA-I	1585
QY	2104	PHLRPLPE---SQPSSSPLLOTAGV---KGHQRVVTLAQHISEVITQDYTRHHPQOLS	2156
DB	1586	TEAGTQPGVSGQVKEGVPVLTSSGAGVFMGRFQVSVAA-----DGAQKGNKS	1636
QY	2157	APLPAPLYFPFPGASCVPDLRRPPSDLYLPPP-----DHGAPARGSPHSEGGKRS	2206
DB	1637	EDAKSVHPESSTSESSVLSSSPESLTVKPEPNGITIPGSSDVPSAHKTTASEAKSDT	1696
QY	2207	PEPNKTS-----VLGGEDGIE-----PVSPPGEMTEPHGSRGAVTPLY	2246
DB	1697	GQPTKVGRFQVTTTANKVGRFVSVKTEDKITDTKKEGCVASPPFMDLEQAVLPAVPKKE	1756
QY	2247	RQEQTEPBRMGSKSPGNTSQP--PAFFSKLTSNSAMVSKKQKQKINKLKNHNRNPEYN	2305
DB	1757	KP-EUSEPRLN-----GPSSDPEAFLSRDVGSGSPHSPHOLSKSL-----PSQN	1804

QY 2306 ISQGTETFINPAITGTLMTYRSQAVQ-----EHA5TNMGLAIIRKALMGKYDOW 2357
Db 1805 LSQSLNSFNSSYMSDNESDIEDLKLELRRLDKHLKEIQDLSRQKHETIESLYTKL 1864
QY 2358 EESPPLSANFNPUNASASIPAAPIITAAQGRSDHTLUTSPGGGKAKVSGRPSRKAQSP 2417
Db 1865 GKVP-----AVIIIPPAPLS---GRRRRPTKS-----KGSKSRSSSLGNKSP 1905
QY 2418 -APGLASGDRPPSV-----SSVHSEGD 2438
Db 1906 QLSGNLSGQSAASVLHPQOTLHPGN 1931
RESULT 66
US-09-854-856-26
; Sequence 26, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 2064
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2064)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-26
Query Match 2.6%; Score 349.5; DB 4; Length 2064;
Best Local Similarity 20.5%; Pred. No. 1.6e-11;
Matches 374; Conservative 187; Mismatches 690; Indels 575; Gaps 81;
QY 822 VPKEEKEETAAAPPVEEGSEQKPPAAEELAVDTGKAEPVKSECTEEAEEGPAKGDAB 881
Db 532 VP-EDVAQEMVESGYVCEGDHKTMAKIKDQVSLIKKKEQROLVREEQEK-----581
QY 882 AABATAGALKAEKKGSG-----RATTAKSGAPQDSDSSATCSAD-EVDEAEGGDKNR 936
Db 582 --KKQESSLIKQVEQSASQTIKQLPSASTGIPTASTTSASVSTQVEPEPEADQHQ 639
QY 937 LLSRPSL-----LPTGD-----PRANASPKPLDLKQKORAA-----IPPI--976
Db 640 LQVQFSISVLSDGTVDGSGSVFTESRVSQOTVSGSQHEQASTGTVPGHIPSTVQ 699
QY 977 ---QVTKVHEPPREDAAPTKAPPAPPNQLPESDAQ-----QPGSSPRGKSRSPAPP 1029
Db 700 AQSQPHGVPPSSVQGIQTAAPPQQTQVYLSQTSSTSEATTAQVPVQPAQVLPQVS 759
QY 1030 ADKEAFAAEAKLPGDPCCWTSGLPPVPREVIVKASHAPDPSAFYAPPGHPLPLGLH 1089
Db 760 AGKQGF-----PPR-----LPQVPGDS--NIAPSSNVASVCIH 791
QY 1090 DTARPVL---PRPTISNPPLISSAKHPSV---LERQICAIQSGMSVOLHVPYSEHAKP 1144
Db 792 ST---VLXPMTEVLATGYFTTVQVYVESNLLVPMGV---GGQVQVSPGGSQAQAP 846
QY 1145 VGVVTMGLPLMPDKKLAPFSGVKQBQLSPRGQAGPPESLGV-----PTAQEASVLRG 1197
Db 847 TTSSQAV-----LESTQGV-----SQVAPAEPVAAQPAQPAQTPTTLASSV--D 888

QY 1198 TALGSPVGGSIITKIGIPSTRVPSDAITYRGSITHGTTPADVLKGTITRIIGEDSPSLDR 1257
Db 889 SAHSDVASG-MSDG--NENVPSSG-----RHEGRTTKHYKRSVRSR 930
QY 1258 GREDSLPGHVIYEGKKGHVLSYEGGMSVTQCSKE-----DGRSSSGPPHET 1304
Db 931 HEKTSRPLRIILNVSKGD-----RVVEQOLETHNRKMWTFKFDLGDN-----PEEI 978
QY 1305 AAPKRYDMMEGRVGRAISSASIEGLMGRAPRERHSPHLLKBOHIRGSIQTGIPRSYV 1364
Db 979 ATIMVNDFI-----LAIERESFVDQVREII---EKADMLSEDSVSEPEGQGL---ESL 1028
QY 1365 EAQEDYLREAKLLKREGTPPPPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRS 1424
Db 1029 QGKDDYGFSGSKLEGEFKOPIASSM-----PQIGIPTSSLTQVHSAAGR 1076
QY 1425 --IHEIPREELRHTELPPLAPRLKEGSIQTGTPLKYDTGASTTGSK-----KHDVRSL- 1476
Db 1077 FIVSPVPSRLRESKVFP-----SEIT-----DTVAASTAQSPGMNLSHSASSLS 1121
QY 1477 -----IGSPGRTFPVPHPLDVMADARALERACYEESLSKSRPG 1513
Db 1122 LQAFSELRAQMTGPNAPPNFSGHTGTFPVVP-----FLSSIAGVPT 1167
QY 1514 TASSGSGSIARGAP-----VIVPELGKPROSL--TYEDHGAPEAGHLPRGSPVTMRE 1564
Db 1168 TAAATAPVATSPNDISTSVIQSEVTVTEGAGVATSGVVTSGGL-----1217
QY 1565 PTPRLOEGLSSSKASQDRKLTSTPREIA--KSPHSTVPEHHHPHPISPYEHLHGRVGV 1621
Db 1218 PIPVSESPVLSVSSVSS-----ITIPAVWSISTTSPSLQVPTSTSEIV-----VSST 1264
QY 1622 DLYRSHIPLAFDPTSPRGICPLDAAAAYVLPRLHAPNTPYHPHYPLI-----1670
Db 1265 ALYPS-----VTVSATSASAGGSTATPGPK-----PPAVSQQAAGSTTVG 1305
QY 1671 -----RGYPTDAALENRO-----TIINDYITSQOMHNTATAMA-----1704
Db 1306 ATLTSVSTTSPSTASQLSIQLSSTSTPTLAEIVVSAHSLDKTSHSTTGLAFSLA 1365
QY 1705 -----QRADMLRGLSPR-----ESSLAANYAAGPRGIIDLSQVPHLPVLP 1746
Db 1366 PSSSSPGAGVSSYISQPGGLHPLVPSVIASTPILPOAAGPTSTPLLPQVPSIPLVQ 1425
QY 1747 TPGTATAMDRLAYLPTAQPPSSRHSRSPSPGCP--THLTKPTTTSSSERERDRDRD 1805
Db 1426 VANVPAV---QOTLHSPQP-----ALLPNQPTHCP-----EVD 1458
QY 1806 RDRREKSLTSTTTTVEHAPIWRPGTEOSSGSSGSSGSSRSPASHSHAHQSPISP 1865
Db 1459 SDTQKAPGIDDIKLEE-----KLRLSFSEHSSGA-----QHASVSL 1497
QY 1866 RQDALQRPSPVLHNTGMKI--ITAVEPSKPTVLESTSTSSPVRPAATFPATHCPGLGT 1924
Db 1498 ETS-----LVIESTVTFGIPTTAVAPSK--LLTSTT-----STCLPPTNLPLG-- 1538
QY 1925 LDGVYPTLMEPVLLPEKAPRVARPRPRADTGHAFKAPPARSGLEPASSPKSEPRPL 1984
Db 1539 -----TVALPVTVPTQGVSTPVSTTSSGVKPGTAFSKPPLTKAP 1579
QY 1985 VPPVSGHATIAKTAKNLAHHASDPDPAPPASADPHREKTQS--KPFISI0ELELRSLGY 2043
Db 1580 VLPVGTETLPAAGTLPSEQL-----PPFPGPSL-----TQSQPLEDLDAQLR---- 1620
QY 2044 HGSSVSPGVEPVSPVSSPLTHDKGLPKHLEELDKSHLEGLRQKQGPVKLGGEAAHL 2103
Db 1621 --RTLSPXITVTSVAV-----KHQHVVTLAQHISEVITQDTRHHPPOLS 2156
QY 2104 PHLRPLPE---SQPSSSPLLQTAQGV---KHQHVVTLAQHISEVITQDTRHHPPOLS 2156
Db 1646 TEAGTQPKGVQVKEGVPVLTSSGAGVFKMGRFQVSAV-----DGAQKEGKNKS 1696
QY 2157 APLPAPLYSFGASCFCVLDLRPPSDLYLPPP-----DHGAPARGSPHSEGGKRS 2206

Db 1697 EDKSVHPESSSESVLSSSESTLVKPEPNGITIPGSSDVPESAHTTTASEAKSDT 1756
QY 2207 PEPNKTSS-----VLGGEDGIE-----PVSPPGEMTEPGHRSRAVYPLLY 2246
Db 1757 GQTKVGRQVTTTANKVGRFVSFKTEKLTDTKKEGPNVSPFMDLEQAVLPVAPVPKKE 1816
QY 2247 RDGEQTEPRMGSKSPGNTSQP-PAFFSKLTESNSAMVSKKQEIINKLKNLTHNRNPEYN 2305
Db 1817 KP-ELSEPHLN-----GPSDDPEAAFLSRDVGSGSPHSPQLSSKSL-----PSQN 1864
QY 2306 ISQPGTEIFNMPALTGTGLMTYRSQVQ-----EHASTNMGLEAIRKALMGKYDQW 2357
Db 1865 LSQSLNSFNSYMSNDSESDIEDLKLRLRDLKHLKEIQDLOSQRQHEIESLYTKL 1924
QY 2358 EESPPLSANAFNPLNASLPAAMPITAADGRSDHTLTSPGGGKAKVGRPSRRKAKSP 2417
Db 1925 GKVPP-----AVIIPPAPLS---GRRRRPTKS-----KGSKSRSSSLGNKSP 1965
QY 2418 -APGLASGRPPSV-----GSVHSEGD 2438
Db 1966 QLSGNLSGQSAASVLHPQOTLHPPGN 1991

RESULT 67

US-09-854-856-56
; Sequence 56, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854, 856
; PRIOR FILING DATE: 2001-05-14
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 2141
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2141)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-56

Query Match 2.6%; Score 349.5; DB 4; Length 2141;
Best Local Similarity 20.5%; Pred. No. 1.7e-11;
Matches 374; Conservative 187; Mismatches 690; Indels 575; Gaps 81;
QY 822 VPKEEKEETAAAPPVEEGEORPPAAEEIADVTGKAEPEVKSECTEEAEEGPAKGDAE 881
Db 472 VP-EDVAQEVESGYVCEGDHKTMAKIDRVSLIKKKEQROLVREEQEK-----521
QY 882 AAEATAGALKAEKKGSGG-----RATTAKSGAPQDSSATCSAD-EVDEAEGGDKNR 936
Db 522 --KKQESSLKQOQESSASQTGIQLPSASTGIPTASTTASVSTQVPEPEADQHQ 579
QY 937 LLSPRSL-----LPTGD-----PRANASPKPLDLKOLKORAAA-----IPPI-- 976
Db 580 LQYQPSISVLSGTVDSGGGSSVFTESRVSSQOTVSYGSQHQEAHSTGTVPGHIPSTVQ 639
QY 977 ---QVTKVHEPPREDAAPTKPAPPAPPONLQPESDAPO---QPGSSPRGKSRSPAPP 1029
Db 640 AQSQPHGVVPPSSVQOGIQGTAPPOQTQVQVLSQTSSTSSSEATTQVPSQVQAPVLPQVS 699
QY 1030 ADKEAFAAEAKLPGDPPCWTSGLPFPVPPPREVIKASPHAPDPSAFSAPPGHPLPLGLH 1089

Db 700 AGKQGF-----PPR-----LPPQYPGDS---NIAPSSNVASVCIH 731
QY 1090 DTARPVL---PRPTTISNPPLISSAKHPSV---LERQIGAISQGMVSQVLHVPYSEHAKAP 1144
Db 732 ST---VLXPEPMTEVLATGYFTVVQPVYESNLLVPMGGV---GGQVQVSPQGSLLAQAP 786
QY 1145 VGPVTMGLPLPMDPKKLAPFGVQKQBLSPRGQAGPPESLGV-----PTAQEASVLRG 1197
Db 787 TTSSQAV-----LESTQGV-----SQVAPAEPAVAQPAQATQPTTLASSV--D 828
QY 1198 TALGSVPGSSITKIPSTRTVPDSAITYRGSITHGTGTPADVLKGTITRIIGEDSPRLDR 1257
Db 829 SAHSDVASG-MSDG--NENVPSSG-----RHEGRTTYKHYRKSVRSSR 870
QY 1258 GREDSLUPKHVITYEGKKGHVLSYEGGMSVTQCSKE-----DGRSSSGPPHET 1304
Db 871 HEKTSRPLRLNVNKGD-----RVVECOLETHNRKWTFFKFDLOGDN---PEEI 918
QY 1305 AAPKRTYDMMGRVGRRAISSASIEGLMGRAPPERHSPHHLKEQHIRGSITQGISRSYV 1364
Db 919 ATIMVNDFI-----LAIERESFVDQVREII---EKADEMLSEDVSVPEGDQGL--ESL 968
QY 1365 EAQEDYLREAKLLKREGTTPPPPPSRDLTEAYKTOALGPLKLPKPAHEGLVATVKEAGRS 1424
Db 969 QGKDDYGFSGSKLEGEFKQIPASSM-----PQIGITPSSLTQVYHSAGRR 1016
QY 1425 --IHEIPREELRHTPLAPRLKEGSITQGTPLKYDTGASTGSK-----KHDVRS-- 1476
Db 1017 FIVSPVPSRLRESKVFP-----SEIT-----DTVAASTAQSGMNLSSHASSLS 1061
QY 1477 -----IGSPGRTFPPVPHPLDMADARALERACYESLSKSRPG 1513
Db 1062 LQAPSELRRQAOWTEGTPNTAPPNFSHTGTPFVVP-----FLSSIAGVPT 1107
QY 1514 TASSSGSITARGP-----VIVPELGKPRQSPL--TYEDHCAQFAGHLPGSPVTMRE 1564
Db 1108 TAAATAPVATSPSPNDISTVTSQSEVTVEEAGIAGVATSTGVTSGGL-----1157
QY 1565 PTPRLQEGSLSSKASODRKLSTPREIA--KSPHSTVPEHHPHPIPSVPHLLRGVSGV 1621
Db 1158 PIPVSESVLSVSSVS-----ITIPAVSISITSPSLQVPTSTSEIV-----VSST 1204
QY 1622 DLYRSHIPAFDPTSIPIRGIPLDAAAAYLPRHAPENPTYPHLYPPYLI-----1670
Db 1205 ALVPS-----VTVSATSAAGSGSTATGPK-----PBAVVSQQAAGSTTVG 1245
QY 1671 -----RGYPDTAALNRQ-----TIINDYITSQQMHNATATAMA-----1704
Db 1246 ATLTSVSTTTSFPSTASQSLISLSSSTSTPTTAEVTVVSAHSLDKTSHSSTTGLAFSLA 1305
QY 1705 -----QADMLRGLGPR-----EGSLALNYAAGPRGIIDLQVPHLPVLVPP 1746
Db 1306 PSSSSSPGAGVSYSIQPGHLPLVIPSVIATPILPQAAGPTSTPLLPQVPSIPLVQP 1365
QY 1747 TPGTPATMDRLAYLPTAPQPFSSRHSPLSPGPG--THLTKPTTTSSSERERDRERD 1805
Db 1366 VANVPV---QOTLIHSQPOP-----ALLPNQPHTHCP-----EVD 1398
QY 1806 RDEREKSILTSTTTVEHAPIWRPGTEQSSGSGSGSGSGSSRRPASHSHAHQHPISP 1865
Db 1399 SDTPKAPGIDDIKTLEE-----KLRSLFSEHSSGA-----OHASVSL 1437
QY 1866 RTQDALQQRPSVLHNTGMKI--ITAVEPSKPTVLRSTSSPVRPAATFPATHCPLOGGT 1924
Db 1438 ETS-----LVIESVTVTGIPTTAVAPSK--LLTSTT-----STCLPPTNLPLG-- 1478
QY 1925 LDGVYPTLMEPVLLPKAPRVARPERPRADTGHAFKAPARSGLPEPASPSKGSBRPL 1984
Db 1479 -----TVALPVTVPVTPGVSTPVSTTTTSGVKPGTAPSKPPLTKAP 1519
QY 1985 VPPVSGHATIAITPAKNLAPHASPDPPAPPASADPHREKTQS--KPFISIOELELSLGY 2043

Db 1520 VLPVGTLPAGTLSEQL-----PPFPSPSL-----TOSQQPLEDLDAQLR----- 1560
Qy 2044 HGSSYSPEGVPVSPVSPSLTHDKGLPKHLEELDKSHLGELRPKQPGVPVKGGEAAHL 2103
Db 1561 --RTLSEXTVTSV----- 1585
Qy 2104 PHLRPLPE--SQSSSPLLQTAGV-----KGHRVVTLAQHISEVITQDYTRHHPQOLS 2156
Db 1586 TEAGTQPKGVQVKEGFLATSSGAGVFWKGRFQVSVAA-----DGAQKEGKNKS 1636
Qy 2157 APUPAPLYSPGASCPLDLRRRPSDLYLPP-----DHGAPARGSPHSEGGKRS 2206
Db 1637 EDKSVHFESSTSESSVSSPSTLVRKPEPNGITIPGISSDVPSAHKTTTASEAKSDT 1696
Qy 2207 PEPNKT-----VLGGGEDGIE-----PVSPPEGMTEPGHRSAAVPLLY 2246
Db 1697 GQTKVGRFOVTTANKVGRFSVKTEDKLTDKKEGFPVSPFMDLEQAVLPAVLPKKE 1756
Qy 2247 RDGEQTEPSRMGSKSPGNTSQP--PAFFSKLTESNAMSVMKSKQEIINKLNTNHRNPEYN 2305
Db 1757 KP-ELSEPSHLN-----GPSDDPEAFLSRDVEDDGSGPSHPHQLSSKSL-----PSQN 1804
Qy 2306 ISQGTIEFNMPALTGLMTYRSQAVQ-----EASTNMGLEAIRKALMGKYDOW 2357
Db 1805 LSQSLNSFNSSNYSNEDIEDDLKLERLRDKHLKEIQDLOSROKHETIESLYTKL 1864
Qy 2358 EESPPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGGKAKVSGRPSRRAKSP 2417
Db 1865 GKVPP-----AVLTPAAPLS---GRRRRPTKS-----KGSKRSSSLGNKSP 1905
Qy 2418 -APGLASGRDPPPV-----SSVHSEGD 2438
Db 1906 QLSGNLSGQSAASVLPHPQOHLHPGN 1931

RESULT 68

US-09-854-856-24
; Sequence 24, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 2201
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)---(2201)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-24

Query Match 2.6%; Score 349.5; DB 4; Length 2201;
Best Local Similarity 20.5%; Pred. No. 1.8e-11;
Matches 374; Conservative 187; Mismatches 690; Indels 575; Gaps 81;
Qy 822 VPKEEKEETAAPPVEEGEOKPPAAEELAVDTGKAEPVKSECTEEAEQPAKGDAB 881
Db 532 VP-EDVAQEMVESGYCEGDHKTMAKAIKDRVSLIKRKEQRLVREEQEK----- 581
Qy 882 AAEATAEGALKAEKKEGGSG---RATTAKSGAPQDSSATCSAD-EVDEAEGGDKNR 936

Db 582 --KKQESSLKQOEQSSASQTGIKQLPSASTGICTASTTSASVSTQVPEPEBEADQHQ 639
Qy 937 LLSPRSL-----LTPTGD-----PRANASQKPLDLKQLKORAAA-----IPPI-- 976
Db 640 LQVQPSISIVSDGTVDGSGSVFTESVSSQQTVSYSQHEQASHSTVFGHIFSTVQ 699
Qy 977 --QVTKVHEPREDAAPTAPAPPQNLPQESDAQ-----OPGSSPRGKRSRPPAP 1029
Db 700 AOSQPHGVPPSPVQOGIOQTAPQOTVOYSLSQTSSEATTAQVSPQAPVLPQVS 759
Qy 1030 AKKEAPAAEAQKLPGDPPCWTSGLPFPVPREVIKASHPADPSAFSAPPAGHPLGLH 1089
Db 760 AKQGF-----LPPQYPGDS--NIAPSSNVASVCIH 791
Qy 1090 DIARPLV--PRPTISNPPLISSAKPSV---LERQICAI SQMSVOLHVPYSEHAKP 1144
Db 792 ST---VLXPPMTEVLATPGYPTVVQPYVENLLVPMGGV--GGQVQVSPGGSQAQAP 846
Qy 1145 VGPVTMGLPLMPDKKLAPFGVKQBLSPRGOAGPPESLGV-----PTAQEASVLRG 1197
Db 847 TTSSQAV-----LESTQGV-----SQVAPAEVAVAAQOATQPTTLASSV--D 888
Qy 1198 TALGSPVPGSITKGIPTSTRVPSDSAITVRGSIHTGTPADVLYKGTITRIIGEDSPRLDR 1257
Db 889 SAHSDVASG--MSDG--NENVPSSSG-----RHEGRTTKRHYRKSVRSRK 930
Qy 1258 GREDISLPKHVIVIEGKGVHLSYEGMSVTQCSKE-----DGRSSSGPPHET 1304
Db 931 HBKTRPKLRIILNVNKGD-----RVVECOLETHNRKMTVFKFDLDGDN----PEI 978
Qy 1305 AAPKRTYDMWEGRVGRAISSASIEGLMGRAPPRHSHPHLKEQHHRGSIQTGIPRSV 1364
Db 979 ATIMVNDFI-----LAIERESFVDQVREI---EKADMLSEDVSVPEEGQGL--ESL 1028
Qy 1365 EAQEDYLRRKALKRREGTPPPPPSRDLTEAYKTOALGPLKLPKPAHEGLVATVKEAGRS 1424
Db 1029 QGKDDYGFSGSKLEGEFKQPIPASSM-----PQIGITPSLTQVHVSAGR 1076
Qy 1425 --IHEIPREELRHTPELPLAPRPLKEGSTQCTPLKYDTGASTGSK-----KHVRSI- 1476
Db 1077 FIVSPVPSRLRESKVFP-----SEIT-----DTVAASTAQSPGMNLSHASSLS 1121
Qy 1477 -----IGSPGRTTFPPVHPVLDVMDARALACRYEESLKRPG 1513
Db 1122 LQAFSELRRAQMTGEPNTAPENFSHTGTPFPVVP-----FLSSIAGVPT 1167
Qy 1514 TASSSGGSIARGAP-----VIVPELCKPROSL--TYEDHGAPFAGHLPRGSPVTWRE 1564
Db 1168 TAAATAPVPATSSPPNDISTSVIOSEVTVPTBEGIAGVATSTGVVTSGL----- 1217
Qy 1565 PTPRLQEGSLSSSKASQDRKLTSTPREIA--KSPHSTVPEHHPHPISPYEHLRGVSV 1621
Db 1218 PIPVSESPVLSVVSS-----ITIPAVVSI STSPSLQVPTSTSEIV-----VSST 1264
Qy 1622 DLYRSHIPLAFDPTSI PRGIPLDAAAAYYLPRLHAPNPTPHLYPPYLI----- 1670
Db 1265 ALYPS-----VTVSATSASAGGSTATPGPK-----PPAVVQQAAAGSTTVG 1305
Qy 1671 -----RGYPDTAALENRQ-----TIINDYTSQOMHNTATAMA----- 1704
Db 1306 ATLSVSTTTPPSTASQLSIQLSSSTSTPTLAETVVVSAHSLDKTSHSTGLAFSLA 1365
Qy 1705 -----QRADMLRGLSPR-----ESSIALNYAAGPRGIIDLSQVPHLPVLPVP 1746
Db 1366 PSSSSSPGAGVSSYISQGLHPLVIPSIVASTPTLPQAGTSTPTLPQVPSIPLVQP 1425
Qy 1747 TGTPTATMDRLAYLPTAPQFPSSHSSSPSPGPG--THLTKPTTSTSSRERDRDRER 1805
Db 1426 VANVPVAV---QOTLIHSQOP-----ALLPNQPHTHCP-----EVD 1458
Qy 1806 RDREKESILSTTTTVEHAPWRPCTEQSSGSSGGGSSSRPASHSHAHQSPISP 1865
Db 1459 SDTQKAPGIDDIKTLLE-----KURSLFSEHSSGA-----QHASVSL 1497

1866 RTODALQORPSVLNHTGMKI-ITAVEPSKPTVLSTSTSSVVRPAATPPATHCPLGGT 1924
1498 ETS-----LVIESVTGIPPTAVAPSK--LITSIT-----STCLPPTNPLIG-- 1538
1925 LDGVYTLMEPVLLPKEAPRVARPERPRADTGHAFIAPKPARSGLEPPASPSKSGSPRL 1984
1539 -----TVALPVTVPVTPGVSTPVSTTTSGVPGTAPSPPLTKAP 1579
1985 VPPVSGHATIARTPAKNLAPHASPPAPPASADPHREKTOS--KPFISIQELLESLSGY 2043
1580 VLPVGTLPAGTLPSEQL-----PPFGPSL-----TOSQPLEDLQLR----- 1620
2044 HGSSYSPGEPVPSVSSPSLTHDKGLPKHLEBLDKSHLEGELRPQKPGVKLGGEAAHL 2103
1621 --RTLSPEXITVTSV-----GPNVMAAPTA-I 1645
2104 PHURLPB-----SQPSSPLLOTAPGV-----KGHVRVVTLOAHISEVITQDYTRHPQOOLS 2156
1646 TEAGTQPKGVQVSGEPVLATSSGAGVFKMGRFQVSVAA-----DGAQKEGKNKS 1696
2157 APLPAPLYSPGACPVLDLRRPPSLYLP-----DHGAPARGSPHSEGGKRS 2206
1697 EDKSVHFSSTSESSVLSSTSPSTLVKPEPNIIPGIISSDVPSAHKTTASEAKSDT 1756
2207 PEPNKTS-----VLGGGEDGIE-----PVSPPGEMTEPGHRSADVPLLY 2246
1757 GQPTKVGRFVTTTANKVGRFSVSKTEDKITDTKKEGVPVASFMDLEQAVLPVAPKKE 1816
2247 RDEQTEPSRMGSKSPONTQOP--PAFESKLTESNAMSVMKSKQEIKNKLTNRNPEYN 2305
1817 KP-ELSEPSHLN-----GPSSDPEAAFLSDVDVDDGSGSPHQLSKSL-----PSQN 1864
2306 ISOPGTEIFENMPAITGGLMTYRSQAVQ-----EHASTNMGLEAIRKALMGKYDOW 2357
1865 LSLSLNSFNSSYNSSDNESDIEDDLKLELRDLKHLKEIODLSRQKHETIESLYTKL 1924
2358 EESPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTPSGGGGKAKVSGRPSRKAQSP 2417
1925 GKVP-----AVIIPPAAPLS-----GRRRRPTKS-----KGSKSSRSSSLGNKSP 1965
2418 -APGLASGRPPSV-----SSVHSGD 2438
1966 QLSGNLSGOSASVLPHPQOTLHPGN 1991

RESULT 69

US-09-919-172-98
; Sequence 98, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 98
; LENGTH: 3256
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 2700132CD1
US-09-919-172-98

Query Match

Best Local Similarity 2.6%; Score 346; DB 4; Length 3256;
Matches 536; Conservative 353; Mismatches 1129; Indels 852; Gaps 133;

QY 4 STQLVAQTRATEPRYPHSLSYVQIARTHTDVGLELYQHHSRD-YAS-----51
DB 325 SVQTPSKAVGASFLYEPAKMKTFFVQYSQQONS-----POKHKNKDLVTTGRRESSVNLGKS 380
QY 52 -----HLSPGSIIOQORRRPSLL-----SEFQPGNERSQELHLRHPESHVLP---EL 95
DB 381 EGFKAGDKTLTPRK-LSTRNRTPAKVEDAADSATKPNLSKSTRGSIPTDVEVLPTETEI 439
QY 96 GKSEMEFIESKPRLELLPDLRLRPSPL-----LATGOPAGS-----EDLTDRSL 141
DB 440 HNEPFTLMTQVERKIQKOSLSKPEKLTAGOMCSGLPGLSSVDINNPGDSINSEGI 499
QY 142 TGKLEPVSPSPHTDEL--ELVPPR-----LSKEELIQNDMDRVDRREITWVEQOI 190
DB 500 PLKRRVS--FGCHLRPELFDENLPNTPLKRGAEPTKRSLVHMTTPVLKIIKEQPQP 557
QY 191 SKLKKKQOOLEB-----AAKPEPEKPVSPPIESKHSRLVQIIYDENRKAEEAARI 244
DB 558 SGKQESGSIHVEVKAQSLVISPAPSPRKTVPVADQRRRSCKTAPASGSKSQTEVPKR- 616
QY 245 LEGLGPOVELPLYNOPSDTROVHENIKINQAMRKKLILYFKRNHA-----RKWKQK 297
DB 617 ---GGERVATCLOKRVISRSQHDILQ-----MICKRSKSGASEANLIIVAKSWDV 664
QY 298 FCORYDQLEALEKKYVERIENPNRRRAKESKVREYIEKQFPEIRKQELQERMQSVQR 357
DB 665 V-----KLGAKTQTKVIKHGPQR-----SMNKQRRRPATPKKPVGEV 702
QY 358 GSGLSMAARSEHEVSEIIDGJSEQENLEKQMRQLAVIPMLYDADQOIRKIFINMGLMA 417
DB 703 HSQFSTGHANSP---CTIIIGKAHTKVVHVPARPYRVLANFI---SNQKMFDEDLGIA 756
QY 418 DPMKVYKDRQVM-----NMWSEOEK--ETEREKFMQHPKNFGLIASFLER-- 460
DB 757 EMPKTVKQPOLSTSTCHIAISNENLKGKFGOTDSGEPLPTSESGCNVFFSAQNA 816
QY 461 -----KTVAECLVYLYLTKQENYKSLVRRSYYRRGKSQQOQQOQQOQQOQQOQMPMR 514
DB 817 AKQPSDKCSASPLRRQCIRENGVNAKTPRNTYKMTSL-----TK 857
QY 515 SSOEKEDEKEKEAEBEKEPEVENDKEDLLKEDTDDTSGEUNDEKAEVASGKRKTANS. 574
DB 858 TSDTETEPSKTVSTVNRSGRSTEFRIQKLVESKSEETNTE---IVECILKRGOKATLL 914
QY 575 QGRKGRITRSMANEANSBEAITPQOSAEIASMELNESSRWTEEMETAKGLLEHGRNW 634
DB 915 QORREGM-----KEIERPPETIK-ENIELKEN-----DEKWKAMKR-----SRTW 954
QY 635 ---SAIARMVGSKTVSQCKNFYFNKKRQNLDEILQOHLKMEKERNARRKKKCAPAAA 690
DB 955 GQKCAPMSDLTDLKSLPDTE-LMKDTARGONLLQ--TQDHAKAPKSEK---KITKMPQS 1009
QY 691 SE-EAAPPVVEDEEMAS-GVSGNEEEMVEEAEALHASG-----NEVPRGEGSGPATVN 743
DB 1010 LOPEINTPTHTKQQLKASLGKVGKVELLAVGKTRTSGTTHTHREPAAGDGKSIRTFK 1069
QY 744 NS-----SDTESI-----PSPHTEAKD--TGQNGP 767
DB 1070 ESPKQILDPAARVTGMKWPRTPKBEAQSLLEDLAGPKELFQTPGPEESMTDKTTKIAK 1129
QY 768 KPPATLGADQPPGPPPTPPRTSRAPTEP-----TPASEATGAPTPPPAPSPSAPP 819
DB 1130 KSPPPESVDTPTSTKQWPKRSLRKADVEBEFLALRLKLTIP-SACKAMLTPKPA-----1180
QY 820 PVPVKEEKEEETAAAPPVE-----EGEEQKPPAAEELA-----VDTGKA 858
DB 1181 ---GGDEKDIKAFMGTPVQKLDIAGTLPGSKROLQTPKKAQALEDLAGKELFQTPGHT 1237
QY 859 EEPV-----KSEC---TEEAEGPAKGD---AEEAATAEALKAEEK---EGSGRA 903
DB 1238 EELVAAGTKTKIPCDSPQSDPVDPTPTSTQORPKRSIRKADVEGELLACRLNMPISAGAMH 1297

Best Local Similarity 18.7%; Pred. No. 4.6e-11;
Matches 536; Conservative 353; Mismatches 1129; Indels 852; Gaps 133;

QY	4	STQLVAQTWATPRTYPPHSLSVPTQJARTHTDVGLEYQHHSD--YAS	51
Db	325	SVQTPSKAVGASFLYPFAKMKTPVOYSOQONS-----PQKHKNKLDYTTGRRRESVNLGKS	380
QY	52	-----HLSPGSIQPORRRPSELL-----SEFQPGNERSQELHLPESHSYLP--EL	95
Db	381	EGFKAGDKTILTPRK-LSTRNRTPAKVEDAADSATKPENLSKTRGSIPTDVEVLPTETEI	439
QY	96	GKSEMEFIESKRPRLELPPPLRLRPSL-----LATQGPAGS-----EDLTQDRSL	141
Db	440	HNEPFLTLWLTOVERKIOKDSLKPEKLGTTAGQCMCSGLPGLSVDINNFGDSINSEGI	499
QY	142	TGKLEPVSPSPPHTDPEL--ELVPPR-----LSKEELIQNMDRVDBREITWVZQOI	190
Db	500	PLKRRRVIS--FGGHLRPELFDENLPPNTPLKRGAPATKRKLSVMHTPVLKIKIKEQPOP	557
QY	191	SKLKKKQOOLEE-----AAKPEPEKPVSPPIESKHSRLVQIIYDENRKAEEAAHRI	244
Db	558	SGQESSETHVEVKAQSLVISPPAPSPRKTIPVASDORRISCKTAPASSKSKSQTEVPER	616
QY	245	LEGLGPOVELPLYNQPSDTRYHENIKINOAMRKKLILYFKRRNHA-----RKOWKQK	297
Db	617	---GGERVATCLOKRVSISRSQHDILQ-----MICKRRSGSEANLIVAKSWADV	664
QY	298	FCORYDOLMALEKKVBERIENPPRRRAKESKVREYEQKFPETRKQBELQERMOSRVQOR	357
Db	665	V-----KLGAQTQTKVIXKHGPOR-----SMNKRRRFPATPKPKPVGEV	702
QY	358	GSGLSMAARSEHEVSEIIDLGSQENLEKQMRQLAVIPMWLYDADQORLIKFINMGLMA	417
Db	703	HSQFSTGHANSP---CTIILGKAHTEKVHVPARPYRVLNNFI---SNQKWDKFEDLSGIA	756
QY	418	DPMKVYKDRQVM-----NNMSEQEK--ETFREKFMQHPKXNFGLIASFLEB--	460
Db	757	EMFKTPVKEQPLTSTCHIAISNSENLLGKQFGQDGSBEPPLLPTSSFCGNVFFSAQNA	816
QY	461	-----KTVAECVLYYLTKKNENYKSLVRSYRRRGKSQOQOQOQOQOQOQOQPMPR	514
Db	817	AKOPSDKCSASPLLRQCIRENGVNAKTPRNTYKMTSLE-----TK	857
QY	515	SSQEBKDEKEKEAEKEEKEPEVENDKEDLLKEKTDOTDGEDNDEKAEVASKGRKTANS	574
Db	858	TSDETPEPSKTIVNRSRGSTERNIOKLVPESKSEETNTE---IVECILKRGQKATILL	914
QY	575	QGRRKGRITRSMANEANSEBAITPOQSAEALASMELNESSRWTEBEMETAKGLLLEHGRNV	634
Db	915	QQRREGEM-----KEIERPFETYK-ENIELKEN---DEKMKAMKR-----SRTV	954
QY	635	-----SATARMVGSKTVSQCKNFYNYKKRONLDEILQOHLKMKERNARRKKKAPAAA	690
Db	955	GQKCAPMSDITDLKSLPDTE-LMKDXTARGONLLQ-TQDHAKAPKSEKG---KITKMPQCS	1009
QY	691	SE-EAAPPVPVVEDEMEAS-GVSGNEBEMVEEAALHASG-----NEVPRGECSGPATVN	743
Db	1010	LQEPINTPHTKQOLKASLGKVGKELLAGVKFTTSGETTHHREPAGDGKSIITFK	1069
QY	744	NS-----SDTESI-----PSPTHEAANKD--TGQNGP	767
Db	1070	ESPKOILDPAARVTGMKKWPRTPKEEAQSLIEDLAGFKELFQTPGFSSEMTDEKTTKIAC	1129
QY	768	KPATILGADGPPGPPPTPPRTSPAPTEP-----TPASEATGATPPPPAPSPSAPP	819
Db	1130	KSPPPESVDPTSTKQWPKBSLRKADVEEBFLARLKUTP-SAGKAMLITPKPA-----	1180
QY	820	PVVPKESKEBETAAAPVE-----EGEEKPPAAABELA-----VDTGKA	858
Db	1181	---GGDEKDIKAPMGTPVQKLDLAGTILPGSKRQLOTPKEKAQAELEDLAGFKELFQTFGHT	1237
QY	859	EEPV-----KSEB---TEFAEBGPAKGD---AENAAEATAEGALKAEEK---EGSGRA	903

1238	Db	EELVAAGKTTKI	FCDSGQSDVDPTTSTKQRPKRSIRKADVEGELLACRNLMSFAGKAMH	1239
904	Qy	TTAKSSGAPODSSSATCSADEYDEAEG--GDKNRLLSPRPSLLTPTGDDPRANASPOKPL	961	
1298	Db	TPKPSVGEKDDIIIFVGTVPQKLDLTENLTGSKRR-----PQTPK	1337	
962	Qy	DLKQLKORAAAIIPIQVTKVHEPPREDAATKPAAPPQPQNLOPESDAPQOGSSPRG	1021	
1338	Db	EEAQALEDLTGFKELFQTPGHTTEAIVAAGKTTKMPCESSPPES-----ADTPTS	1386	
1022	Qy	KSSPAPPADKEAFAAE-----AQKLPGDPPCWTSGLPFPVPPREVIKA	1065	
1387	Db	TRRQPTPLEKRDVQKELSAKLLKLTQTSGETTHTDKVPGEDKSNAF-----RETAK-	1439	
1066	Qy	SPHAPDPSAFSAPPQHP-----LPLGLHDTA-----RVLPRPPTTISNPPPLISSAKH	1114	
1440	Db	--QKLDPAASVTGSKRPKTKERAKQPLEDLAGWKELFQTPVCTDKPTTHEKTTKIACRSQ	1497	
1115	Qy	PSVLERIQIGAISQMSVOLHVHPYSE-----HAKAPVGPVTMGLPLP--MDPKKLAPPSGV	1167	
1498	Db	PDPVDPTTSKQSKRSLRKVDVEEBFFALRKETPSAGKAMHTPKPAVSGEKNIIAFMGT	1557	
1168	Qy	KQSQLS--PRQAGPPESGLVPTAQEASVLRGTLGSLVPGGSIITKGIPTSTVPDSAITYR	1226	
1558	Db	PVKQLDLENTLTSKRRLQTPKE-----KAQALEDLAG---PKELFQTRGHTEE-----	1603	
1227	Qy	GSITHGTPADVLKYGITRIIGEDSPSRLDRGREDSLPKGHVIEGKKGHVLSYEGGMSV	1286	
1604	Db	--SMTNDKTAACKSQPDL--DKNPASSKRLKTSLGK-----VGVEKELLAVG---KL	1652	
1287	Qy	TQCSKEDGRSSGPPHE-----TAAKRTYDMGREGVRGIRATSSASIEGLMGRAIPPER	1339	
1653	Db	TQTSGETTHTEPTGDKSMKAFMESPKQILDSAAASLTG---SKRQLRTPKGKSEVPED	1709	
1340	Qy	-----HSPHLKEQHHRIGSIT--QGIPRSVVEAQEDYLRREAKLLKBECTGPPPPP	1389	
1710	Db	LAGFIELFQPSHTKE-----SMTNEKTTKVSIRASQPD-----LVDTTPTSSKQP	1755	
1390	Qy	SRDLTEAYKTQALGPLKLKPAHEGLVATVKE---AGRSIHEIPREELRHTPELPLAPRPL	1446	
1756	Db	KRSLRKA-----DTEEFLEAFKQTSAGKAMH-----TPKPA	1788	
1447	Qy	-----KEGSITQGTPL-KYDTGASTTSGKKH-----DVRSLIGSGRTPFP	1486	
1789	Db	VGBEKOINTPLGTPVKQLDQPGNLPGSNRRLQTRKEKAQALEELTFRELFQTPCTDNPT	1848	
1487	Qy	V-----HPLDMADA-----RALERACYEBSLSRPGCTASSSGSIARGA	1526	
1849	Db	TDEKTTKKILCKSPQSDPADPTINTKQRPKRSLUKKADVEEFLEAFKRLTPSAGKAMHTPK	1908	
1527	Qy	PVTIYPE-----LGKPRQSPLTVEDGAPAGHLPRGSPVTMEPTPRLOEGSLSSKAS	1580	
1909	Db	AANVEEKDINTFVGTPVEK-----LDLLGNLP-GS--KRPPQTPK-----ERAKAL	1951	
1581	Qy	QD-----RKLTSPT-----REIA-KSPHSTVPEHHHPHPIISYEHLLRGVSGVDL	1623	
1952	Db	EDLAGFKELFQTPGHTTEESMTDDKITEVSCSKSPQ---PDPVKPTSSKQRLKISLGKVG	2008	
1624	Qy	YRSHIPLA-PDPTSIIRGPIPLDAAAAYLPRHLAPNPTYPHLYPPYLIRGVPDTAALENR	1682	
2009	Db	KEEVLVPGKLTQTS-----GKTTQTH-----R	2030	
1683	Qy	QTTINDITYTSQOMHNTATAMARQDMLRGL-----SPRESSLALNYAAGPRGIIDLSQV	1737	
2031	Db	ETAGDG--KSIKAFKSAKQMLDPANVGTGMEWRPRTPKAEASQLEDLAGFK---ELFQT	2085	
1738	Qy	P-HLPLVLPPTPGTPATMDRLAYLTPAQPFSSRSHSSPLSPGPGTHLTKPTTTSSSR	1796	
2086	Db	PDHT-----EESTTDDKTTKIACKSP-----PESMDTPTST---R	2118	
1797	Qy	ERDRDRDRDRREKSI---LTSITTVEHAP-----IWRPGTEQSSGSGSGSGG	1845	
2119	Db	RRPKTPILGKRDIIVEELSALKQLTQTHTDKVPGEDKGINVFRETAKQLDPAASVTG--	2176	

Qy	1946	GSSSRPASHAHQHSPI	SPTDQALQORPSVLHNTGMKII	TAVEPSKPTVLRRSTSTS	1904	
Db	2177	-----SKRQPRTPKGAQPLEDL	--AGLKELFOTPICTDPTTHEKT-TK	2218		
Qy	1905	SPVPEAATFPATHCPLGGTL	DGVYPTLMBP-----VLLPKEAPRVARP-	1948		
Db	2219	IACRSQDDPVGT-----	PTIFPQSKRSIRKADVEEESIALRRKTPSVGKAM	2366		
Qy	1949	ERPRADTG-----	HAFLAKPAPRSGLEPASP	SGSEPRPLVP-----PVSGHATIA	1995	
Db	2367	DTPCAGGDEKMAFGMT	PQVKLDL--PGNLP--GSKRWQTPKEKAQAL	EDLAGFKELF	2323	
Qy	1996	RTPAKN-----	LAPHASDDPAPPASADSPHREKTQSKPFSIQE	--LELRSLGY	2043	
Db	2324	QTPTGDTPTTDEKTTK	LACKSPQDPDVTASTK--QRPRNLRKADVEE	EFLALR----	2377	
Qy	2044	HGSSYSPEGVEPSPVSS	PSLTHDKGLPKHLELDKSHLGELRPKQGPVKLG	GERAAHL	2103	
Db	2378	---KRTPSAGKAMD--	TPKPAVSDKENDINTFET-----PVQKLDLIGNL	2417		
Qy	2104	PHLRPLESOFSSSPLLQ	TAPGVK-----CHORVVTLAGHISEVITQD	-----YTRH	2150	
Db	2418	PGSKRQQTPEKEAEAL	EDLVGFKELFQTPCHTEESMTDKITEVSCSKS	PQPSFKTSRS	2477	
Qy	2151	HPQQLSAPLPAPLYSP	FGASCPVLDLRRPP---SDLVLPDPD---HGAPARSPHSEGG	2303		
Db	2478	SKQRLKIPLVK-----	VDMKEEPLAVSKLRTSGETTQTHTEPTGDSKGIKAF	2525		
Qy	2204	KRSPE---PNKTSVLGGED	-----GLEP-VSPPEGWTBPGHSRS	AVPPLYRDGE	2250	
Db	2526	KESPKQILDPAASVTG	RRQLRTRKEKARALDVLDFKELFSPAGHTEESM	-----T	2577	
Qy	2251	QTEPSRMGSKSPGNTS	OPAFFSKLTESN	AMVSKKQEI	INKLNTHNRNEPEYNISQPG	2310
Db	2578	IDKNTKIPCKSP-----	PPELTDATSTKCPKTLRKEVKEELSAVERLT	--QTSQGS	2629	
Qy	2311	TEIFNMMAITGTLMTYR	SQA-----VOEHAS-----	2337		
Db	2630	THTHKEPASGDEGIK	VLQKRAKKPNPVEBEP	RRRRPRAPKEKAQPLEDL	AGFTELSETS	2689
Qy	2338	--TNWGLEAIRKALMG	KYDWE--ESPPLGANAFNPLNASAL	-----P	2378	
Db	2690	GHTQESLTA-----	GKATKIPCESPLEV-----VDTTASTKSHLRTVQKVQVKEEP	2737		
Qy	2379	AAMPITAADGRSDH	TLTSPGGGKAKYSGRPPSRKAKSPAPGLASGRPP	2428		
Db	2738	SAVKFTQTSGETT	DADPEAGEDKGIKALKE	SAKOTPAAPASVTGSRRP	2787	

RESULT 71

US-09-854-856-46

00-03-034-030-40
; Sequence 46. Application US/09854856

; sequence 40, Appl
; Patent No. 6541252; FACEID NO. 6341232
; GENERAL INFORMATION:

APPLICANT: walke. D. Wade

APPLICANT: WATKE, D. WADE
APPLICANT: HILBUN ERIN

APPLICANT: HILBUN, ERIK

APPLICANT: DOHONO, Gregory
APPLICANT: Turner, C Alexander Jr

APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: NO 6541252ol Human Kinases and Polymers of actin

1. TITLE OF INVENTION: Encoding the same

; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: I.F.V.-0170-USA

FILE REFERENCE: LEX-0178-USA

; CURRENT APPLICATION NUMBER: US/0

;; CURRENT FILING DATE: 2001-05-14

;
PRIOR APPLICATION NUMBER

; PRIOR FILING DATE: 2000-

; NUMBER OF SEQ

; SOFTWARE: FA

; SEQ ID NO 4

; LENGTH: 2076

; TYPE: PR

QY 874 -----PAKGDAAEABATAGALKAEKKEGGGRATTAKSSGAPQSDSDSATCSADEVDE 928
Db 1160 TPGPKPPAVVQQAAGSTTVGATLTSTVSTTSPSTASQSLQSLSSTSTPTLAETVWVS 1219
QY 929 AEGGDKN-----RLTSP-----RSLTPTGDPANAS----- 956
Db 1220 AHS�DKTSHSTTGLAFSLAPSSSSPGAGVSSYISQPGHLPLVPSVIASTPILPOA 1279
QY 957 -----PQKDLKQKQRAAAIPPIQVTKVHBPREDAAFTKPAAPPQPPQNLQP 1007
Db 1280 AGPTSTPLLPQVP-SIPPLVQPVANPAVQOTLIHSQOPALLPNQPHTHCPVEDSDTQP 1338
QY 1008 ESAPQOPG-----SSPRGKSRPAPPADKEAFAAEAQKLPQBPCCWTSG 1052
Db 1339 KA-----PGIDDKITLLEKRLSFSEHSSGASHVSLSLTSVIBSTVTPGIPPT---- 1389
QY 1053 LPFPVPPREVIKASPHAPDSAFSAPPCHPLPLGLHDTARPVL--RPTISNPPPLIS 1110
Db 1390 ---AVAPSKLL-----TSTTSTCLPPTNLPLG--TVALPVPVTPVQGVSTPSTVTT 1436
QY 1111 SAKHPSVLERQIGAIISQGMVOLHVPSYEHAKAPVGPVTMGLPLPMDP-KKLAPFSG--V 1167
Db 1437 SGVKGPTAPSK-----PPLTKAPVLPGVTELPAGTLPSEQLPFPFGPSL 1480
QY 1168 KQEQ-----LSPRG-----OAGPPESLGVPTA-OEA-----SVLRGTAL 1200
Db 1481 TOSQOPLDLDLAQRRLTSLPEXITVTSVAVGPFVSMAPTAITEAGTQPKGVSOVKEGPVL 1540
QY 1201 GSVPGGSITK-GIPSTRVPSDSA-----ITYRGS-----ITHGTADVLVK 1240
Db 1541 ATSSGAGVFMGRFQVSVAAADQAKGKNKSEDAKSVHFPESTSSSVLSSSPSTLVK 1600
QY 1241 ----GTTITRIIGDSP-----SRLDRGDSLPGKHVYEGKKGHLVSEYGMVS 1286
Db 1601 PENGTITPISDSDVESAHTTASEAKSDTGQTKV-----GRFQV 1642
QY 1287 TQCKEDGRSSGPPHETAAPKRYTDMGVRGAISSASIEGLMGRAIPPERHSHHLK 1346
Db 1643 TTTANKVGRFSVKTED---KITDTKCGPVA-SPPFMDLEQAVLPAPVIPKEKP-ELS 1696
QY 1347 EQHHRGSIQGIIPRSYVQAEQYLLREAKLLREGTPPPPPSRDLTEAYKTQALGPLK 1406
Db 1697 EPSHLNG-----PSSDPEAA--FLGRDVD--DGSGPSHSPHQLSSKSLPSONLSQSL 1744
QY 1407 LKPAHEGLVATVKEAGRSIHEIPRELRHTPELPAPRPLKEGSIQTGTPLYKDYTGASTT 1466
Db 1745 SNFSNYSMSDNES-----DIEDDLK-----LELRDRDKHLKEIQDLQ----- 1785
QY 1467 GSKKHVRSILIGPGR-----PPVHPLDVMADARALERACYEESLKSRLP-----GTASS 1517
Db 1786 SRQKHEIESLYTKLGVPPAVIIPPAAPL-----SGRRRPTKSKGSKSS 1830
QY 1518 SGSGIARGAPVIVPELKGKPRQSPLYTHEDHAGPAGHLPRGSPVTMPREP-----T 1566
Db 1831 RSSSLGNKSPOLSGNLSGGSAASVLHPQOQLHPGNIPESGQNLLOQLKPSPSNDLYS 1890
QY 1567 PRLOEGLSSKASQDRKLTSTPREIAKSPHSTVPEHPH 1605
Db 1891 APTSDGAISVPSLSAPCGQTSNTVTGATVNSQAAQAP 1929

RESULT 72

US-09-854-856-14

; Sequence 14, Application US/09854856

; Patent No. 6541252

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Hilbun, Erin

; APPLICANT: Donoho, Gregory

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides

; TITLE OF INVENTION: Encoding the Same

; FILE REFERENCE: LEX-0178-USA

; CURRENT APPLICATION NUMBER: US/09/854,856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 2136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2136)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-854-856-14

Query Match 2.6%; Score 343.5; DB 4; Length 2136;

Best Local Similarity 18.8%; Pred.No.3.7e-11;

Matches 346; Conservative 245; Mismatches 731; Indels 517; Gaps 74;

QY 100 MEFIESKRPRLELLPDPL-----LRPSPLLATGQPAGESDL-----TKDRSLTGKLEPVS 149
Db 335 LQFLHTRTP-----PIIHRDLKCDNIITG-PTGSVKIGDLGLATLKASPAKSVIGT 386
QY 150 PPSPPHTDPELELVPPRLSKEELIQMDRVDRITVWEOQISKLKKKQOOLEE----- 203
Db 387 P-----EFMAPEMYEERYDESVDVYAFGCMLEMATSEYPYSECQNAAQIYRRVT 436
QY 204 -AAKPEPEKPVSPPIE-----SKHSLV011-----YDENRKKAAEAHRILEG 247
Db 437 SGVKPASDFKVAIPEVKEIIEGCIQNKQDERYSIKDLNLHAFQEETGVRVELAE---ED 493
QY 248 LQPOVELPLYNOPSDTROVYHENIKINQAMRKKLILYFKERNHARKQWKQKFCOR----- 301
Db 494 DGEKIAIKLWLRIEDIKLKGKYNKNEAIE---FSFDLERDVPDVAQEMVSEGVYCEG 549
QY 302 -YDQLEALEKKVERIENPNRRRAKESKRYEYKOFPE---IRKQREIQERMQSRVQOR 357
Db 550 DHKTMAKAIKDRVSLIK--RKREQQLVREOEKKQKQESSLKQVQESSASQTGKQL 606
QY 358 GSG-----LSWSAARSEHEVSEIIDGLSEQENLEKQMLAVIPMLYDADQORIKFIN 411
Db 607 PSASTGIPTASTTSASVSTQVPEPEADQHOQLOQPSISVLSOGTVDSGGSSVFTE 666
QY 412 MGLMADPMKVYKDRQVMNMWSEQEKETPREKFMQHPKNF--GLIASFLERKKTVAECVLY 469
Db 667 SR-----VSSQQTVSYSQHEQ-----AHSTGTVPCHIPISTVQAQSQPHGV-- 707
QY 470 YLTKKNENYKSLVRRSYRRRGKSGKQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 519
Db 708 YPPSSVAQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQ 767
QY 520 KDEKEKEKAEEKEEKEPEVENDKEDL-----LKEKTDITSGED---N 558
Db 768 ATTAQVSPQFQAPQVLPQVSAGKSTQGSQVAPAEFVAQQAQTPTTLASVDSNHS 827
QY 559 DEKEAVASKRKTANSQGRKGRIT-----RSMANEANSEEAITPQOSAEASLAMELNESS 613
Db 828 DVASGMSDGNENVPSSSGRHEGRTTKRHYRKSVRSRHEKTSRPKLRILNVS---NKGD 884
QY 614 RMTTEEMETAKKGLLE-----HGRNWSAIAARMVGSKTVCQKQNFYNYKQKQNLDEILQ 668
Db 885 RVVECCQETHNRKMWTFKFDLDGDNPEEA-----TIMVNDPILAIERSEFVDQV--- 935
QY 669 HKLKMEKERNARKKKKAPAAASEEAAPFVVEDEBMEA-----SGVSGNES----- 715
Db 936 -----REIIEKADEMLSEDSVSEF-EGDQGLLESQKDDYFGFSQKLEGEFKQ 983
QY 716 -----EMVEE-----AEALHASGNEVPGRCSGPATVNNSSDTESTIPSPHTE----- 757
Db 984 PIPASNPQOIGIPTSSLTQVHSAG-----RRFIVSFVESRLRESKVPFSEITDVAAS 1039
QY 758 AAKDTQNGFKPPATLG-----ADGPPFPPTPPRRTSRAPTEPTPASEATG 804

Db 1040 TAQSPGMNLSHSSLSLOAQSELRAQMTGENTAPNFSTGPTFPVVPFLSSIAQ 1099
QY 805 APTPPAP---PSPAPP-----PVPKEKEETAAA-----PPVER 839
Db 1100 VPTAAATAPVATSPNDISVTSQSEVTVTEGIAGVATSGVTVSGGLPIPVSE 1159
QY 840 G-----EQKPPAABELAVDTGKABEPVKSECTEABERG--- 873
Db 1160 SPVLSSVSSITIPAVVSIITSPSLQVPTSTSEIVVSSHTALVPSVTVSATASAGSTA 1219
QY 874 -----PAKGKDAABAATAGALKAEKKEGSGRATTAKSSGAPQDSGASATCSADEVDE 928
Db 1220 TPGKPPAVVQQAAGSTTVGATLTSVTSITTSFPSTASQLSIQLSSSTSTPTLAETVWVS 1279
QY 929 AEGGDKN-----RLLS-----RPSLLTPTGDPNANAS----- 956
Db 1280 AHSLDKTSHTSTGLAFSLGAPSSSSPGAGVSYISQPGHLPLVIPSIVASTPILPOA 1339
QY 957 -----PQKPLDLKQKRAAAIPIQVTKVHEPPREDAAPTKPAAPPAPPPQNLQP 1007
Db 1340 AGTSTPLLPQVP-SIPPLVQPVANVPVAVQOTLIHSQPQALLPNQPHTHCEVDSDTQP 1398
QY 1008 ESDAPOQG-----SSPRGKSRPAPPADKEAPAAEAQKLPDPPPCWTS 1052
Db 1399 KA-----PGIDDIKTLEKLSLFSHSSGAGHASVLSLETSLVIESVTTPGIPTT--- 1449
QY 1053 LPFPVPPREVIKASPHAPDSAFSAPPCHPLPLGLHDTARVLP--RPTTNSNPPPLS 1110
Db 1450 ---AVAPSKLL-----TSTTSTCLPTNPLG--TVALPVPVTVPGQVSTPVSTTT 1496
QY 1111 SAKHPSVLERIQIGAIISQGMVQLHPYSEHAKAPGVPTMGLPMDP-KKLAPFSG--V 1167
Db 1497 SGVKPGTAPSK-----PPLTKAPVLPVGTETLPAQTLPSQQLPFPGPSL 1540
QY 1168 KQIQ-----LSPRG--QAGPPESLGVPTA-QEA-----SVLRGTAL 1200
Db 1541 TQSQQPLEDLDAQLRRTLSPXITVTSVAVGPFVMAAFTAITAGTQPKGVSVKQEGPVL 1600
QY 1201 GSVPGGSITK-GIPSTRVPSDSA-----ITVRGS-----ITHGTADVLVK 1240
Db 1601 ATSSGAGVFKMGFRQFVVAADGAKQKGNKSEDAKSVHFESSTSSSVLSSSPSTLVK 1660
QY 1241 ----GTHIRIIGBSP-----SRLDRGREDSLPKGHVYIEGKGHVLSEYEGMSV 1286
Db 1661 PEPNGITIPGSSDVPESAHKTTASEAKSDTGQTKV-----GRFQV 1702
QY 1287 TQCKSKEDGSSGPPHETAPKRTYDMGVRGVAISSASIEGLMGRATPERRHSPHLK 1346
Db 1703 TTTANKVGRFSVSKTED---KITDTKGGPVA-SPPFMDLEQAVLPVAPKKEP-ELS 1756
QY 1347 EQHHIRGSITQGIPTRSVVEAQEDYLAREAKLLKREGTPPPPPSRDLTEAYKTOALGPLK 1406
Db 1757 EPSHLG-----PSSDPEAA--FLSRVDV---DGSQSPHQPUSKSLFSONLSQSL 1804
QY 1407 LKPAHEGLVATKEAGRSIHEIPRELRHTPELPLAPRLKESITQGTPLKYDTGASTT 1466
Db 1805 SNSFNSSVYSSDNES-----DIEDEDLK-----LELRRLDKHLKEIQDLQ----- 1845
QY 1467 GSKKHVRSLIGSPGT-----PPVHPLDWDADARALERACVEESLKRSP-----GTASS 1517
Db 1846 SRQKHEIESLYTKLGVPPVPAVIPPAPL-----SGRRRRPTKSGSKSS 1890
QY 1518 SGSGIARGAPVIVPELPGKPRQSPLTVEDHGAPAGHLPRGSPVTMREP-----T 1566
Db 1891 RSSLGNKFPQISGNLSGASASVLPQOTLHPGPNIPESGQNLQPLKPSPSDNLSY 1950
QY 1567 PRLOEGSLSSKASQDKRLTSTPREIAKSPHSTVPEHP 1605
Db 1951 AFTSDCAISVPSLSAPGQGTSTSTNTVGTATVNSQAAQAP 1989

US-07-741-940-2
; Sequence 2, Application US/07741940
; Patent No. 5352775
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: MAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/741,940
; FILING DATE: 19920109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.035574
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2843 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-741-940-2

Query Match 2.6%; Score 343.5; DB 1; Length 2843;
Best Local Similarity 17.7%; Pred. No. 5.4e-11;
Matches 472; Conservative 356; Mismatches 1005; Indels 829; Gaps 108;
QY 50 ASHLSFGSIQIP--ORRRPSLLSEFQ-----PGNRSQELHLRSHSY 91
Db 740 ANIMSPGSLPSLHVKKQKALEAELDAQHLSSETFNIDNLSPKASHRSKQRHKQSLYGDY 799
QY 92 LPELCKSMETESKRPRLLELLPDLPLRPSPLATGQAPAGSEDLT---KDRSL----- 141
Db 800 VPDTRHRDNKSDNFTNGMTVLSYLTNTVLPSSSSRSGSLDSSRSKDRLEERIG 859
QY 142 TOKLEFPVSPPPHTDPELELVPPLRSKEELIQNMDRVDRITMVVEQOISKLKKQOOLE 201
Db 860 LGNYHPATEN-----PGTSSKRGK-----QISTTAAQIAKV-----ME 892
QY 202 EBAKPPPEKPPVPPPIESKHSRSLVQIYYDENR--KKAEAHRLLEGPGOVELPLVNO 259
Db 893 EVSAIHTSQEDRRSGSTTE-----LHCVTDERNALRESSAAH-----THSNTYN- 936
QY 260 PSDTRQYHENIKINQAMRKLILYFKRRNHARKQWKQKFCQRYDOLMEALEKKVERIENN 319
Db 937 --FTKSENSTCSMPYAK---LEYKRSSN-----DSL-----NSVSSNDGY 973
QY 320 PRRRAKESKVREYEEK-----QFP-EIRKQRELOERMQSRVQGRSGLSMSAARSE 369

Db 974 GRGQMKPSIESSEDESFCYSQYQPADLAHHSANMDDNDGELDTPIYSLKYSYD 1033
QY 370 HEVSEIIDGLSEENLEKQMRQLAVIPMLYDADQORIKFINMGLMADPMKYKQOVQM 429
Db 1034 -----EQLNSGRQ-----SPSQNERWARPKHIIIEIKOSEQORQR 1069
QY 430 NMWSEB--KETPREKFMQHPKNGFLIASFLERKTVAECVLYLYLTKBNYKSLVRSY 487
Db 1070 NQSTTVPVYTESTDDKHLKQPHFG-----QQECVPSYRSGANGSETNRVGSNH 1119
QY 488 RRRGKSOOQOQOQOQOQOQOQPMPSRSEDEKDEKEKE-----AEKEBKPVEVD 541
Db 1120 ---GINQVNSQSLCOEDDYDDKPTNYSERYSSEEQHEEERPTNYSIKYNEBKHVDQ 1176
QY 542 KEOLLKEKT-----DTSGEDN--DEKEAVASKRGKRTANSQGRKGRITRSM 587
Db 1177 IDYSLKYATDIPSSQKQSFSSKSSQSQSKTEHMSSENTSTPSSNAKRONQLHPSSA 1236
QY 588 NEANSEAITPQOASLAMELINESRWTEEMETAKGGLLEHGRNWSAIARMVSGKTVS 647
Db 1237 QSRSGQ---PQAAATCKVSSINQETIQTVCVEDTP-----ICFSRCSLSLS 1281
QY 648 QCKNFYNYKRONLD--EILQOHKLW--KERNARKKKKAPAAASEEAAFPVVEDEE 704
Db 1282 SADEIGCNQTTQEADSANTLQIABTKIGKIGTRSAEDPVSEVPAVSQH-----PRTKSSR 1336
QY 705 MEASGVSGNEE---EMVEEAEALHASGNEVPRGE---CSGPATVNNSSDTESTPSP 754
Db 1337 LQSSLSSESARHAKAVEFPSCAKSPSKSGAOTPKSPPEHVQETPLMFSRCTSVSLDSF 1396
QY 755 HTBAKXDTGQNGPKPATLADGP-----PPGPPTTPRRTSRAPIBPTPASEATGPTTP 809
Db 1397 ESRSIASSVQSEPCSGMVSGIISPSDLDPSPGQTMPPSRK-----TPP 1440
QY 810 PAPSPSAPPVPVKEKEEETAAAPVBERGEQKPPAAEELAVDTGKA---EPPVKSEC 866
Db 1441 P-PPOTAQTKREVFPKNK-----APTAEKRESGPKQAAVNAAVQVQLPDAADTLHFA 1492
QY 867 TEABEEG-----PAKGKDAEAEATAEGALKAKEGGSGRATTA---KSSGAPQDSD 916
Db 1493 TESTPDGFCSSLSALSULDEPIQKDVLRIMPPVOENDNGNETSEQKESNENQKE 1552
QY 917 SSATCSA--DEVDEAEGD---KNRLSPRSLTPTGDPNANASPKPLDLKQLKQRA 970
Db 1553 AEXTIDSEKDLDDSDDDDIIELECIIISAMPT-----KSSRGKKP-----AQTA 1598
QY 971 AAIPTQVTKHEPPREDAAAPTAPAPPONQOPESDAPQOQSS--PRGKSRPAPP 1029
Db 1599 SKLPPPVARKPSQLPVYKLLPSQ-----NRLQPKHVFTPGDDMPR-----1640
QY 1030 ADKEAPAAEAQKLPDPPCWTSGLPFPVPPREVIKASHPADPSAFYAPPGHPLPLGLH 1089
Db 1641 ---VYCVG-----TPINFSTA-----TSL 1658
QY 1090 DTARPVLPRPPTISNPPPLISSAKHPSVLBRQIGAISQMGVQLHVPYSEHAKAPGPT 1149
Db 1659 DL-----TIESRP-----NELAAGEVGGAGQSGEFEXKRDITPT- 1692
QY 1150 MGLPLMDPKLAPFSGVQKQESLPRQAGPPPSLGV-----TAQASVLRGTALGSVP 1204
Db 1693 -----EGRSTDEAQGGKTSVITIPELDDNKAEEGDILAECSAMP 1733
QY 1205 GG-----SITKGIPTRPVSDSAITYR---GSIHTGTPADVLYKGTITRII 1247
Db 1734 KGSKHPRFRVKIMDQOQASASSAPNKLQDKKKKPTSPVKPIPONTETRYTRVK-- 1791
QY 1248 GEDSPRLDRGRDLSLPKGHVIEGKKGHVLSEGGMSVTCQSKED---GRSSSGPPHET 1304
Db 1792 NADSKNNLNAERVSDNK-----DSKKQNLKNNSKDFNDKLPNNEDRVGRSGFAFDSPHH- 1845
QY 1305 AAPKRTYMMMEGRVGRRAISSASIEGL-----MGRAIIPPRHSPHLLKEQHHRGSIT 1356

Db 1846 -----YTRIETPYCFSRNDSLSLDFDDDDVDLSR-----EKAEELKAKENKESAKVT 1895
QY 1357 QGIPRSYVBAEDYLREAKLLKREGTPPP-----PPPSRDL-----TEAYKTOA 1401
Db 1896 SHTELTSNQSANKTOAIKQPINRGOPKPILOKQSTFFQSSKDIIPDRGAATDEKLQNFA 1955
QY 1402 LGPLKULKPAHEGLVATVKEAGRSIHIEIPREELRHT-----PELPAPRPLKBSGITO 1453
Db 1956 IENTPVCFHNSLSLSLSDIQENNNKENEPIKETBPPDQSGEPSPQASGYAPKSPHVE 2015
QY 1454 GTPKLYDTCASATTG-----SKKHVRSLSIGSPRT 1483
Db 2016 DTPVCFSRNDSLSLSDIEDLLQECISSAMPKKKPKRLKGNDEKSPNNMGILGE- 2074
QY 1484 FFPVHPLDVMADARALERACYEESLSKSRPCTASSGSGSIARGAPVTVPELKGKPRQSP 1543
Db 2075 -----DLTLDLKDIOQPDSEHGLS--PDSENFDMKAIQEGANSIVSSL-----2115
QY 1544 EDHGAFFAGHLPR-----GSPVTWREPTPLQEGSLSSSVASQDRKL 1585
Db 2116 --HQAAAAACLSQAOSDSDSLKSGSIGSLGSPFHL---TPQEEKPFTSNKG-----2164
QY 1586 TSTPREIAKSPHSTVPEHHPHPISPYEHLLRGV--SGVDLYRSHIPLAFDPTSPRGIPLD 1644
Db 2165 ---PRILKPECKSTL-----ETKLTESKGIKGGKVKYS-----2197
QY 1645 AAAAYLPHRLAPNTYPHLYPIRLIRGYPDTAALENRQTIINDYITSQOMHHTATAMA 1704
Db 2198 -----LITG-----KVRNSEISGOM-----2213
QY 1705 QRADMLRGLSPRESSIALNVAAGPRGIDLSQVPHLPVLVPPTPGTATAMDRLAYLPTA 1764
Db 2214 -----KQPLQANMPSISRG---RTMIHIPGV-----2236
QY 1765 PQPFSSRSHSSPLSPGCPHLLTKPTTSSSERDRDRDREREKSLTSTTT---1820
Db 2237 ---RNSSTSTSPVSKGKGP--LKTPAKSPSEGO-----TATSPRGA 2274
QY 1821 -----VEHAPIWRPGTEQSGSGSGSGSGSGSRPASHAHQHSPISPRTOALQORP 1875
Db 2275 KPSVKSELSFVARQ--TSQIGGSKAPSRGSRDSTPSRPAQQLSRPIQSPGRNSI---2329
QY 1876 SVLHNTGMKGIITAVBPSPKPTVLRSTSTSPVRPAATFFPATHCPLGGLTUDGVYP- 1930
Db 2330 ---SPGRNGI---SPPNKLSQLPRTSPSTA-----STKSGSGKMSYTPSGRQMS 2374
QY 1931 --TLMEPVLLPKEAPRVARPERPRADTGHAFKAPPARSCLEP-----ASSPSKGE- 1980
Db 2375 QONLTQOTGLSKNASSI-----PRSESASKLQNMNGNANKKVELSRMSSTKSGSES 2429
QY 1981 ---PRPLVPVSGHATIAITPA--KNLAPHASDPDPAPPASADPHREKTQSKPFSIQEL 2036
Db 2430 DRSERPVLVROSTFFIKEAPSPTLRRKLEESASFESLSPSRPASPTRSQAT--PVLSPSL 2488
QY 2037 EURLGYHGSSYSPGVEPVSPVSSPSLTHDKGLPKHLELDKSHLEGEURPKQPGPVKL 2096
Db 2489 PDMSLSTH--SSVQAGGWRKLPNLSPTIEYNDGRPAKRHDIAARSHSESPSRL----PINR 2543
QY 2097 GG--EAHLPLRPLPESQPSLPLQTAGVKGHVVTLAQHISEVITQDYTRHHPPQ 2154
Db 2544 SGTWKEKSKH-----SSSLPRVSTWRRTGSSSILSSESSEKASEKDEK----2591
QY 2155 LSAPLPAPLYSPFGASCVPDLRRPPSLDLPDPDHGAPARGSPHSGGSRSPENKTS- 2213
Db 2592 -----VNSISGK-----QSKENQVSAKGTWRKIKENEFPTNSTSQ 2628
QY 2214 -VLGGEDGIE-----PVSPPGEMTEPHGSRSAVYPLLYRDEGEQTEPSRMGSKPNTS 2266
Db 2629 TVSSGATNGAESKTLIYQMAPAVSKTEDVMVRIEDCPI-----NNPRSGRSPGTNT- 2679
QY 2267 QPAPAFSKLTESAMVSKKQKQINKLNTHNNEPEYNISQPGTEIFNMPAITGTGLMT 2326
Db 2680 -PP-----VIDSVSEKANPNIKDSKDNQAKQNV-----GNGSVP 2712

! INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2843 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-452-654-2

Query Match 2.6%; Score 343.5; DB 1; Length 2843;
 Best Local Similarity 17.7%; Pred. No. 5.4e-11;
 Matches 472; Conservative 356; Mismatches 1005; Indels 829; Gaps 108;

QY 50 ASHLSPGSIQIP--QRRRLSLSEFQ-----PENERSOELHLRPESHYSY 91
 DB 740 ANIMSPGSSLSPLSHVRKQKALELDAHLSETFDNIDNLSPKASHESKQRHKQSLGYD 799
 QY 92 LPELGKSEMFIESKRPRLLELDPDLPRLPPLATGQAGSEDLT---KDRSL----- 141
 DB 800 VFDNRHDDNRSONFNTGNMTVLSFYLNTVLPSSSSRGLSDSSRSEKDRSLERERGIG 859
 QY 142 TGKLEPVSPSPPTDPELELVPRLSKBELIQNMDRVREITWVEQOISKLKKKQOOLE 201
 DB 860 LGNVHPATEN-----PCTSSKRL-----QISTTAAQIAKV-----ME 892
 QY 202 EBAKPEPEKPVSPPIESKHSRLVQIIYDENR--KKAEEAAHRILEGLPQVPELPLYNQ 259
 DB 893 EVSAIHTSQBDRSSGSTTE-----LHCVTDERNALRRSSAAH-----THSNTYN- 936
 QY 260 PSTDQVHENIKINQAMRKLLILYFKERNHARKQWKQFCQRYDQLMLEALEKKVERIENN 319
 DB 937 --FTKSENSNRTCSMPYAK--LEYKRSSN-----DSL-----NSVSSNDGY 973
 QY 320 PRRRAKESKVREYEEK-----OPP-EIRKQRELQERMQRVQSGSLGSSMSAARSE 369
 DB 974 GKGQMKPSTESYSEDDSEKFCYGVQYPADLAHKHSANHMDDNGELDTPINYSKYSD 1033
 QY 370 HEVSEIIDGLSEENLEKQMLQALVPPMLYDADQRIKFINNGLMADPMKVYKDRQWM 429
 DB 1034 -----EQLNSGRQ-----SPSQNERWARPKHIIIEIKQSEQRQSR 1069
 QY 430 NMWSEQE--KETREKFMQHPKNGFLIASFLERKTVAEKVLVYLLTKKNENYKSLVRSY 487
 DB 1070 NQSTTPVYTESDHHKLFQPHFG-----QQECVSPYRSGANGSETNRVGSNH 1119
 QY 488 RRGKSQQQQQQQQQQQQQQQQMPRSPQEEKEKEKE-----AEKEEKEPVEVD 541
 DB 1120 ---GINQVNSQSLQEDDDYDKPTNYSERYSEEQHEEERPTNYSIKYNEEKRHVDQ 1176
 QY 542 KEDLLAKETD-----DTSGEDN-DEKEAVSKGRKTANSQGRKGRITRSMA 587
 DB 1177 IDYSLYATDIPSSQKQSFSSKSSGQSKTEHMSSESTSTPSSNAKRNQNLHPSSA 1236
 QY 588 NEANSEAITPQOASLAMELNESSRWTEEMETAKGGLLEHGRNWSAIARMVGSKTYS 647
 DB 1237 QSRSGQ----PQAAACKVSSINQETIQYCVEDTP-----ICFSRCSSLSUS 1281
 QY 648 QCRNFYNYKRNQND--EILQOHKLME--KERNARRKKKAPAAASEEAPFPVVEDEE 704
 DB 1282 SAEDEIGCQNTQEADSAANTLQAEIKGKIGTRSAEDPVSEVPVAVSQH-----PRTKSR 1336
 QY 705 MEASGVSGNEE-----EMVEAEALHASGNEVPRGE-----CSGPATVNSSDTESIPSP 754
 DB 1337 LQSSLSUSSSARHKAVEFFSGAKSPSKGATPKSPPEHYVQETPLMFRSCTSVSLDSF 1396
 QY 755 HTEAAKDTQNGPKPATLADGP-----PPGPTPTPRRTSRAPTEPTPASEATGAPTP 809
 DB 1397 ESRSIASSVQSEPCSGMVSGIISPSDLPDPSQGTMPSPRSK-----TPP 1440
 QY 810 PAPPSAPPPVVPKEKEEETAAAPVEEGEBQKPPAAEEELAVDTGKA---EEPVKSEC 866
 DB 1441 P-PPQATQKREVPKNK-----APTAEKRESGPKQAANVAQVQVLPDADTLLHFA 1492
 QY 867 TBEAEEG-----PAKGDAEAAEATAEGALKAEKKEGSGRATTA---KSSGAPQDS 916

DB 1493 TESTPDGFCSSSLSALSLEDEPIQKDELIMPVQENDNGNETESEQPKESNENQKE 1552
 QY 917 SSATCSA--DEVDEAEGD-----KNRLSPRSLLTPTGDPDRANASPOKPLDLKQLKQRA 970
 DB 1553 AEKTIIDSEKDLLDDSDDDIEILEECIIISAMPT-----KSSRKGKKP-----AQTA 1598
 QY 971 AAIPTPIQVTKVHEPPREDAAPTAPPPQNLQOPESDAPQOCSS--PRGKSRSPAPP 1029
 DB 1599 SKLPPPVARKPSQLPVYKLLPSQ-----NRLQPKHVSTPDDMPR----- 1640
 QY 1030 ADKEAFABAQKLPGDPPCWTSGLPFVPREVIRKASPHAPDPSAFSAPPGHPLPLGLH 1089
 DB 1641 ----VYCVGEG-----TPINESTA-----TSL 1658
 QY 1090 DTRAPVLPPTTINPPPLISSAKHPSVLEROIGALSQMSVOLHVYPYSEHAKAPVGPVT 1149
 DB 1659 DL-----TIESPP-----NELAAGEVGRGAQSGEFKRDITPT- 1692
 QY 1150 MGLPLPMDPKLAPFSGVKQEOLSPRGOAGPESLGPV-----TAQEAASVLGCTALGSVP 1204
 DB 1693 -----EGSTDEAOGKTSSTVPIPELDDNKAEEDILAEICINSAMP 1733
 QY 1205 GG-----SITKGIPSTRVPSDAITYR-----GSITHGTADVLYKGTITRII 1247
 DB 1734 KGKSHKPFVRVKIMDOVQOASASSAPNKNQLDGKKKPTSPVKPIPQNTYRTRVK-- 1791
 QY 1248 GEDSRLDRGREDLSLPKHVHYEGKKHVLVYEGMSVTCQSKED---GRSSGPPHET 1304
 DB 1792 NADSKNNLNAERVFSDNK-----DSKQNLKNNSKDFNDKLPNNEDRVGRSGFAFSPHH- 1845
 QY 1305 AAPKRTYDMWGRVGRATISSASIEGL-----MGRAPPRHSPHHLKEQHHRGSI 1356
 DB 1846 -----YPIEGTFCFSENDSLSLDFDDDDVLSR-----EKAELRKAKEKSEAKVT 1895
 QY 1357 QIGIPRSYVQAEQDYLRREAKLLKREGTPPP-----PPPSRDL-----TEAYKTOA 1401
 DB 1896 SHTELTSNQOASANKQAIKQINRGQPKPILOKQSTFPQSSKDIPIRGAATDEKLQFPA 1955
 QY 1402 LGPLKLPAGEGLVATVKEAGRSIHEI PREELRHT-----PELPLAPRLKEGSI 1453
 DB 1956 IENTPVCFSHNSLSLSLSDIDQENNNKNEPIKETEPDPSQGEPSKPOASGVAPKSFHVE 2015
 QY 1454 GTPLKYDTGASTTG-----SKQHDVRSLSIGSPGT 1483
 DB 2016 DTFVCFSRNSSLSSLSIDSEDDLQECISSAMPKKKPSRLKGDNEKHSPRNMGGILCB- 2074
 QY 1484 FFPVHPLDMADARALERACYEESLKSRRPGTASSGGSIARGAPVIVPELGHKPROSPLTY 1543
 DB 2075 -----DLTLDLKDIQRPDSEHGLS--PDSENFDMKAIQEGANSIVSSL----- 2115
 QY 1544 EDHGAPFAGHLPR-----GSPVTMREPTPRLQEGSISSSKASQDRKL 1585
 DB 2116 --HQAAAAACLSRQSSDSLSLSKSGISLGSFPFH-----TPDQEEKPFTSNKG----- 2164
 QY 1586 TSTPREIAKSPHSTVPEHHHPHPISEYHLLRGV--SGVDLYRSHIPLAFDPTSIPIRGILPD 1644
 DB 2165 ---PRILKPGEXSTL-----ETKKIESEKGIKGGKVKYS----- 2197
 QY 1645 AAAAYLPHLAPNTYPHLYRGVPTAALENQOTINDYITSQMHHTATAMA 1704
 DB 2198 -----LITG-----KVRNSNSEISGQM----- 2213
 QY 1705 QRADMLRGLSPRESSALNAAAGPRGIIDLQVPHLPVLVPTPTGTATAMDRLAYLPTA 1764
 DB 2214 -----KQPLQANMPSISRG-----RTMHI PGV----- 2236
 QY 1765 POPFSRRSSSPLSPGGPHTLTKPTTSSRRERDRDRDREREKSIITSTTT----- 1820
 DB 2237 ---RNSSSSTSPVSKGPP-LKTPASKPSRQ-----TATTSRGA 2274
 QY 1821 ----VEHAPWRPTEQSSGSSGSSGSSGSSRSPASHAHQHSPISPRITQDALQORP 1875

Db 2275 KPSVKSELSVARQ-TSQIGSSKAPSRGSRDSTPSRPAQQLSRPIQSPGRNSI-----2329
QY 1876 SVLHNTGMKGIIITAVBFSKPTVLRSTSTSPVRPAATFPFPAHCPGLGTLDDGYVP-----1930
Db 2330 -----SPGRNGI-----SPENKLSQLPRTSSPSTA-----STKSSGSGKMSYTSPPGRQMS 2374
QY 1931 --TLMPEVLLPKAPRVARERRADTGHAFKAPPARSGLEP-----ASSPFGKSE-1980
Db 2375 QONLTKQTGLSKNASSI-----PRSESASKGLQNMNGNGANKKVELSRMSSTTKSSGES 2429
QY 1981 ---PRPLVPVSGHATTIARTPA-KNLAPHASDPDPAPPASADPHREKTQSPFISQEL 2036
Db 2430 DRSERPVLRQSTFIKEAPSTLRRKLESASFESLSPSRPASPTRSQOT-PVLSPSL 2488
QY 2037 ELASLGVHSGSYSPGVEPVSPVSSPLTHDKGLPKHLELDKSHLEGELRPKQPGVKL 2096
Db 2489 PDMSLSTH-SSVQAGGWRKLPNLSPTIEYNDGRPAKRHDIAHSHSPSRL-----PINR 2543
QY 2097 GG--EAAHLPHLRPLPESQSSPLLOTAPGVKGHORVVTIAQHISEVITQDTRHHPOQ 2154
Db 2544 SGTWKEHSHK-----SSSLPRVSTWRRRTGSSSSILSASSESEKAKSEDEKH-----2591
QY 2155 LSAPLAPLYSFPGASCPVLDLRPPSDLYLPPDHGAPARGSPHSEGGKRSPEPNKTS-2213
Db 2592 -----VNSISGTK-----QSKENQVSAKGTWRKIKENEFPTNSTSQ 2628
QY 2214 -VLGGEDGIE-----PVSPPGCMTEPGHRSAGVPLLYRDGEQTEPGRMGSKSPNTS 2266
Db 2629 TVSSGATGAESKTLIYQMAPAVSKTEDVWVRLEDCEPI-----NNPRSGRSPGTNT-2679
QY 2267 QPPAFPSKLTESAMVSKKQINKLNTNHNREPEYNIQPGTEIFNMPATITGLMT 2326
Db 2680 -PP-----VIDSVSEKANPNIKSDKNQAKQNV-----GNGSVP 2712
QY 2327 YRSQAVQEHASTWGLEAIIRKALMGKYDQWESPPLSANAF-----NPLNASASLPAAM 2381
Db 2713 MRTVGLNRLTFSIQDAPDQKTEIKPGQNNPVVSETNESPIVERTPSSSS-----2767
QY 2382 PITAADGRSDHTLTSPPGGGKAKVSG---RPSSRKAKSPAPGLASGRDPPSVSHSEGD 2438
Db 2768 -----SKH--SSPSGTVAARVTTPNPNPSRKSSAD-----STARSQIIP-----2806
QY 2439 CNRRTPLTNRWEDRPSAGST 2460
Db 2807 ----TPVNNNT-KKRDSTKTDST 2823

RESULT 76
US-08-370-235A-2
; Sequence 2, Application US/08370235A
; Patent No. 5910418
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: HILL, DAVID E.
; APPLICANT: JOHNSON, KAREN A.
; TITLE OF INVENTION: ANTIBODIES AND ASSAYS FOR DETERMINING
; TITLE OF INVENTION: MUTATIONS IN THE APC GENE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,235A

; FILING DATE: 01-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.48688
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508 9100
; TELEFAX: 202 508 9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2843 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-370-235A-2

Query Match 2.6%; Score 343.5; DB 2; Length 2843;
Best Local Similarity 17.7%; Pred. No. 5.4e-11;
Matches 472; Conservative 356; Mismatches 1005; Indels 829; Gaps 108;

QY 50 ASHLSPGSIQIP--QRRRPSLLSEFQ-----PCNERSOELHLRPESHYSY 91
Db 740 ANIMSPGSSLP SLHVRKQKALEAEADQHLSETFDNIDNLSPKASHRSKORHKQSLYGDY 799
QY 92 LPGLKSEMEFIESKRPLELLPDP LRLPSPLATQGPAGSEDLT---KDRSL-----141
Db 800 VPDNRHNDNRSDNFTGNMTVLSPYLNTTVLPSSSSRSGSLDSSRSEKDRSLERERGIG 859
QY 142 TKLEPVSPSPHTDPELELVPRLSKBELIQNMORVDREITWVQQISLKKKKQQOOLE 201
Db 860 LGNYHPATEN-----PGTSSKRGL-----QISTTAAQIAKV-----ME 892
QY 202 EAAKPEPEKPPPPPIESKHSLVQIIYDENR--KKAEEAHRILEGLGPQVELPLYNQ 259
Db 893 EVSAIHTSQEDRSSGSTE-----LHCVTDERNALRRSSAAH-----THSNYTN- 936
QY 260 PSDTROYHENIKINQAMRKKLILYFKRRNHARKQWKQFCQRYDQLEALEKKEKVERIENN 319
Db 937 --FTKSENSNRICMPYAK--LEYKRSN-----DSL-----NSVSSNDGY 973
QY 320 PRRRAKESKVRREYK-----QFP-EIRKQRELOERMQRVQQRSGSLMSAARSE 369
Db 974 GKRQMKPSIESYSEDESKFCYQYPADLAHKIHSANHMDDNDGELDTPIYSLKYSYD 1033
QY 370 HEVSEIIDGLSEQENLEKQMRQLAVIPMLYDADQQRKIFINNMGMLMADPMKVYKORQVM 429
Db 1034 -----BOLNSGRQ-----SPSQNERWARPKHIIEDIKOSEQRQSR 1069
QY 430 NMWSEOE--KETFREKFMQHPKNFGLIASFLERKTVACVLYYLTQKNENYKSLVRSY 487
Db 1070 NQSTTYPVYTESTDDKHLKFPHFQ-----QQECVSPYSRGANGSETNRVGSNH 1119
QY 488 RRRGSKQQQQQQQQQQQQQQQPMRPSQERKDEKEKE-----AEKEEKPEVEND 541
Db 1120 --GINQNVQSILCOEDDYEDDKPTNYSEYSEEEHEEERPTNYSIKYNEKRVHDQP 1176
QY 542 KEDLLKEKTD-----DTSGEDN-DEKEAVASKRKTANSQGRKGRITRMA 587
Db 1177 IDYSLKYATDIPSSQKQSPFSKSGSGSKTEHMSSESTSTSPSSNAKRONQLHPSSA 1236
QY 588 NEANSEEAITPQCSAELASMEINSSRWTEEMETAKGILLEGHNRWSAIAARMVGKTSVS 647
Db 1237 QSRSGQ----PQKAATCKYSSINQETIQYCVEDTP-----ICFSRCSLSLSLS 1281
QY 648 QCKNFYNYKKRQNLD--EILQOHKLKME-KERNARRKKKKAPAAASBAAPFVVEDEE 704
Db 1282 SADEITGCNTQOADSANTQIAETIKGIGTRSAEDPVPSEVPAVSOH-----PRTKSSR 1336
QY 705 MEASGVSGNEE-----EMVEEAALHASGNEVPRGE-----CSGPATVNNSDTSPSP 754
Db 1337 LQSSLSSESARHKAVEFPFSGAKSPKSGAQTPKSPPEHYQETPLMFRCRTSVSLDSF 1396

2016	DTPVCF	SNSLSLSIDSEDDILQECISSAMPKKKXPSRLKNGNEKXHSPRNMGILGE-	2074
1484	FPVHP	LDVMDADARALACRYEESLKRPGTASSGGSGIARGAPVIVPELCKPRQSPITY	1543
2075	-----	-DLTLDLKDIOQPDSEHGLS--PDSENFDWAKIQEGANSIVSSL	2115
1544	EDHGAP	FAGHLPR-----GSPVTWREPTPRLOEGSLSSKASQDRKL	1585
2116	--HQAAAA	ACLRSQASDSILSKGSLGSPFHL--TPDQEEKPFTSNKG-----	2164
1586	TSTPRE	TAKSPHSIVPEHHPPISPYEHLRGV--SGVDLVRSHIPLAFDPTSTPRGIPLD	1644
2165	--PRILK	PGESKTL-----ETKKISESGIKGKKVYKS-----	2197
1645	AAAA	YILPRHLAPNPTYPHLYPRGYPDTAALENROTIIINDYITSQQMHHNTATAMA	1704
2198	-----	-LITG-----KVRNSEISGOM-----	2213
1705	QRADML	RGLSPRESSLALNYAAGPRGIIDLSQVPHLFVLVPPPTGTPATAMDRLAVLPTA	1764
2214	-----	-KQPLQANPMSISRG--RTMIHIFGV-----	2236
1765	POPSS	RHSSPLSPGPGTHLTKXTTTSSEERDRDRDRDREREKSIILTSTTT-----	1820
2237	--RNS	SSTSPVSKKGP-LKTPASKPSEGO-----TATTSPRGA	2274
1821	-----	-VSHAPIWRPGTQSGSSGSSGGGSSSRPASHAHQHSPISPRTODALQORP	1875
2275	KPSVKS	LSLSPVARQ--TSQIGSSKAPSRSGSRUSTPSRPAQPLSRPIQSGRNSI----	2329
1876	SVLHNT	CMKGIITAVEPSKPTVLSTSTSPVRPAATFPFATHCPLGGLTLDGVYP-----	1930
2330	-----	-SPGRNGI---SPENKLSQLPRTSSPSTA-----STKSSGSKMSYTPSGRQMS	2374
1931	--TLME	VLLPKEAPRVARPERPADTGHAFILAKPAPRSGLEP-----ASSPSKGSE-	1980
2375	QONLT	KOTGLSKNASSI-----PRSESAGKLNQMNNGANKKVELSRMSTSKSGSES	2429
1981	-----	-PRPLVPVPSGHATTARTPA--KNLAPHASPDPPAPPASADPHREKTQSKPFSIQEL	2036
2430	DRSER	VLVQSTFIKEAPGFTLRRKLEESASFESJSPSRPASPRTSRQAT--PVLSPSL	2488
2037	ELRSL	YHGSSYPGEVPEVSPVSSPLSTHDKGLPKHLEBDSKSHLEGLRPRQPGPVKL	2096
2489	PDMSL	STH--SSVQAGGWRKLPNPLSPITIEYNDGRPAKRHDIAHSSESPSRL----	2543
2097	GG--EA	AHLPHLRPLPSQSSPPLQTAGVKGHORVVTLAQHSIVTQDVTRIHPQO	2154
2544	SGTW	KRHSKH-----SSSLPRVSTWRTTSGSSSILSASSESSEKAKSEDEKH----	2591
2155	LSAPL	PAPLYSPFGASCFLVLDLRPPSDLYLPDPHCAPARGSPHSGGKSGSEPNKTS-	2213
2592	-----	-VNSISGTK-----QSKENQVSAKGTWRKIKNEFSPSTNSTSQ	2628
2214	-VLGG	GDGIE-----PVSPPEGMPTEPGHRSADVPLLYRDGEQTEPRMGSKSPGNTS	2266
2629	TVSSGA	TNGAESKTLIIYQMAPAVSKTEDVWVRIEDCPI-----NNPSPSGESPTNT-	2679
2267	QPAPF	SKLTESNAMYKSKQEIKNKLNTNNEPEYNIISQGTIFINMPAITGTGLMT	2326
2680	-PP-----	-VIDSVSEKANPNIKDSKNQAKQNV-----GNGSVP	2712
2327	YRQAO	QEHASTNMGLEAIRKALMGKYDQWESSPPLSANAF-----NPLNASASILPAAM	2381
2713	MRTV	GLENLRTSIFIQVADPDQKTEIKPGQNNPVPVSETNESPIVERTPFSSSSS-----	2767
2382	PITAAD	GRSDHLLTSPGGGKAKVSG---RPSSRKAKSPAGLASGDRPPSVSSVHSEGD	2438
2768	-----	-SKH--SSPSGTVAARVTPNNYNSPRKSSAD-----STCARPSQIP-----	2806
2439	CNRRT	PLTNVRWEDRPSAGST	2460
2807	----	-TPVNNNT--KKRDSKTDST	2823

Qy	1639	RGIPLDAAAAYVLP	PHRIAPNPTPHLY	PPVLI	RCY	PDPTALE	NRQTTI	NDYIT	TSQQMHHN	1698	
Db	1275	SSSSPGAGVSYISQ	-----PGGLHPLV	PSVI	-----	-----	-----	-----	-----	1302	
Qy	1699	TATAMAQRADMLRGL	SPRESSLALNYAAG	PRGIIDLSQV	PHLPVLV	PPPT	PGCTATAM	DRL	1758		
Db	1303	-----	-----ASTPIL	POAAGT	STP	LLPOV	PSIP	PLVOP	VANPAV	-----QQ	1341
Qy	1759	AYLPATAPQPPSSRHSS	PLSPGGB	-THLT	KPTTTSS	SE	RRDRDRDRDR	DREREK	SILTS	1817	
Db	1342	TLIHSQPQP	-----ALLP	NPHTCP	-----	-----	-----	-----	-----	1377	
Qy	1818	TTTVEHAPIWRPGTEQ	SSGSSGGGGSSRR	PASHASHAHQHS	PISPR	TDALQQR	PSV	1877			
Db	1378	IKLUEE	-----KLRS	LFSEHSSGA	-----	-----	-----	-----	-----	1409	
Qy	1878	LHNTGMKG1-I	TAVEPSKPTVL	STSTSSPVR	PAATFP	PPATHC	PLGGLT	DGVVPTL	MEPV	1936	
Db	1410	IESVTGPIPTTA	VAPSK--LLT	STT	-----	-----	-----	-----	-----	1445	
Qy	1937	LLPKEARVARPER	PRADTGHAF	LAKPAP	ARGLE	PASSPSK	GSEPR	PLVPVPSGH	ATIA	1996	
Db	1446	-----	-----TV	ALPVTV	PPVTV	PGQVST	TTTSGV	KPGTAP	KPLTKAP	VLVPLV	1498
Qy	1997	TPAKNLAPHAS	PDPPAPPASAD	PHREKTS	-KPF	SIQ	IELRSL	GYHSS	SPGCV	2055	
Db	1499	LPSEQ	-----	-----PP	PGPSL	-----	-----	-----	-----	1537	
Qy	2056	VSPVSSPLTHDKGL	PKHLEL	DKSHLE	GBUR	PKQOP	GVKLG	GBAAHL	PHLR	PLPE	2112
Db	1538	TSAV	-----	-----	-----	-----	-----	-----	-----	1564	
Qy	2113	QPSSSPLLOTAPGV	-----KG	HORVVV	TLAQH	ISEVIT	ODYTRH	HPQQL	SALPLAP	LYSPFG	2168
Db	1565	QVKEG	PLVATSSGAGV	FNGR	QVSVAA	-----	-----	-----	-----	1615	
Qy	2169	ASCPVLDLRPP	SDLYLPPP	-----	-----	-----	-----	-----	-----	2213	
Db	1616	SESSVLS	SSPESTLV	KPEPNG	ITPG	ISSDV	PESAHKT	TA	SEAKS	DTGQTKVGR	1675
Qy	2214	-----	-----VL	GGEGD	IE	-----	-----	-----	-----	2258	
Db	1676	TTANKGRF	SVSKTE	KITDT	KEG	VASPP	FMDO	EQAV	PAV	IPKKEK	1734
Qy	2259	SKSEGT	SQP-PAP	FSKL	TESN	AMVKS	KQ	EQIN	KLNT	HRNEPE	2317
Db	1735	-----	-----GP	SSDPEAA	FLSR	DVDDG	SGSPHS	PHQL	SSKSL	-----	1783
Qy	2318	AITGTGLM	TVRSQAVQ	-----	-----	-----	-----	-----	-----	2369	
Db	1784	YMSSDN	SEDEDE	LKLELR	RLRDK	HLKE	TDQL	QS	RQKH	IESLYTK	1836
Qy	2370	PLNASIL	PAAMP	ITAA	DGRSD	HTLTP	SGGG	GKAK	VGR	PSRRKAK	2428
Db	1837	-----	-----AV	IPPA	APLS	-----	-----	-----	-----	1884	
Qy	2429	SV-----	-----SS	VHSEG	D	2438					
Db	1885	SVLHP	OOTLHP	PPGN	1898						

RESULT 82

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RES001 82
US-09-854-856-62
; Sequence 62, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; FILE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA

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QY 2169 ASCVLDLRPPSLYLPPP-----DHGAPARGSPHSEGGKSPFPNKTS----- 2213
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1616 SESSVSSSPSTLVKPEPNIIPGISSDVPESAHKTTASEAKSDTQPTKVRQVPT 1675
QY 2214 -----VUGGEDIE-----PVSPPEGMTEPHGSRSAVYPLLYRDEGOTEPSPRMG 2258
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1676 TTANKVGRFVSKEDEKITDTTKGPGVASPPFMDLEQAVLPVAPVKKKEP-ELSEPSHLN 1734
QY 2259 SKSPGNTSQP-PAPFESKLTSNSAMVSKKQETINKLNTNHRNEPEYNIOPGTEIFNMP 2317
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1735 -----GPSDEFAFLSRDVGSGSPHQLSSKSL-----PSNLSQSLSNSFNSS 1783
QY 2318 AITGTGLMYRSQAVQ-----EHASTNMGLEAIRKALMGKYDQWESPPLSAMAFN 2369
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1784 YMSSDNESDIEDEDLKLELRRLRDKHLKEIQDLSQROKHEIESIYTLGKVP----- 1836
QY 2370 PLNASASLPAMPTAADGRSDHTLTSPGGGGKAKVSGRPSRKAQKSP-APGLASGRPP 2428
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1837 -----AVIIPPAAPLS-----GRRRRPTKS-----KGSKSSRSSSLGNKSPQLSGNLGQSA 1884
QY 2429 SV-----SSVHSEGD 2438
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1885 SVLHPQOTLHPPGN 1898

RESULT 84
US-08-963-825-20
; Sequence 20, Application US/08963825
; Patent No. 6110689
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/963,825
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/187,319
; FILING DATE: 21-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
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```
? CLONE: COLLAGEN -ALPHA 1 (II)
US-08-963-825-20

Query Match      2.5%; Score 330.5; DB 3; Length 1418;
Best Local Similarity 20.4%; Pred. No. 1.2e-10;
Matches 378; Conservative 117; Mismatches 631; Indels 727; Gaps 86;

QY 721 AEALHASGNEV-----PRGECSPATVNNSSDTHESIFSPHTEAAK-----DTGONG-P 767
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18 AAVLRCCQGDVROPKQKQKGBPGDIKDIVPKPGPGQPGAGEQGRGDRGDKBKGAP 77
QY 768 KP-----PATLGADGP--PPGPPPTPP-----RRTSRAP 794
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
78 GPRGRDGEFTLGNPCCPGPPGPPGLGNNFAAQWAGGDFEKAGGAQLGVWQGMGPM 137
QY 795 EPTPASEATGATPP-----PPAPSPSAPPVVPVKEEKEETAAAPVVEEGEEQKPPAA 848
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
138 GPRGPPGAPAGAPQPGFQGNPGEPGEPGVSQGMGPR-----GPP---GPPGKPG-- 183
QY 849 EELAVDTGKAERPVKSECTEEAEERGPAKGDAAEAATAEGALKAKEKGGSGRATTAKS 908
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 -----DDGAGKPGKA-----GERGPPQPGARGFPPT-PGLPGVKGHRGYPLDCAKGE 232
QY 909 SCAPQDSDSSATCSADEVDEAEAGGDKNRLLSRPSLLTPTGDPANASQKPLDLKQLKQ 968
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
233 AGAP-----GVKGE-----SGSPGENGSP-GPMGPRGLPG 261
QY 969 RAAAPPIQVTKVHEPPREDAAPTAPAPPPPPQNLQPESDAPQPPGSS----- 1018
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
262 ERGRTGFPAGAAGAR---GNDGQFGPAGPFGPVGAGPGFPGAGKAGAGTARGPGE 318
QY 1019 ---PRGKSRSPAPPADKEAFAAEAKLPGDPPCWTSGLFPVPPREVIVKASHAPPSAF 1075
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
319 AQCPGPGTTPGSPG-----PAGASGNPG-----TDGIP-----GAKGSAGAPGIA-- 359
QY 1076 SYAPPGHPLPLGLHDTARPVLPPTTISNPPPLISSAKHPSVLERIQGIAISQMSVOLHV 1135
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
360 --GAPFGPGRG-----PPD-----PQG----- 375
QY 1136 PYSEHAKAPVGPV-TWGLPLPMDPKLAPFSGVQEOQLSPRQAGPPESLGVPTAGEASV 1194
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
376 -----ATGLPGKQGTGKP-----GIAGFKGEQ-GPKGEPGAGPQAGPAGAGEG 420
QY 1195 LRGTALGVPGGSIITKGIPISTR-VPSDSAITVRGSI--HGTADVLYKGTITRIIGDS 1251
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
421 KEG-ARGE-PGGVGPPIGPPGERGAPGNRGFPQDGLAGKPGAP-----GERG 465
QY 1252 PSRL-----DRGR--EDSLPKGHVIVEGKKHVLVSEGGMSVTQCSKEDGRSSSGPP 1301
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
466 PSGLAGPKGANGDPRGPPEPLPGARGL-TGRPGDA-GPQKVKVSPGAPGEDGR--PGPP 521
QY 1302 HETAA-----PKRTYDMMGRVGRA-----ISSASIEGLMGR-----AIPPER 1339
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
522 GPQAGARGQGVVMGFPFGKA-----NGEPKAGEKGLPGAPGLRGLPGKDGTCAGGPPGP 577
QY 1340 HSPHLKEQHIRG-SITQGIPIRSYVEAQEDYLRREAKLLKREGTPPP-----PPSRDL 1393
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
578 AGPAGERGEQAGAPPSGFGLP-----GPPGPPGEGKPGDQGV 616
QY 1394 T-EAYKTQALGPL-----KLKAHEGLVATVVEAGRSIHEIPREELRHTPELAPLR 1444
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
617 PGEAGAPGLVGRGRGFRGFRGERSGPAQGL-----QGPRGLFGTGTGDKGASGAPGPP 671
QY 1445 PLKEGSIITQGTPLKYDTGTATTSKKHD-----VRSLSIGSPOR-----TFPPVPLDVM 1493
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
672 GAQGPGLQGMPP--GERGAAGTAGPKGRDGVGEKGPAGKDGGRGLTIGIFPGPAG 729
QY 1494 ADARALERACYEESLKSRPGTASSSGSIRAGAPVIVPELGPQRSPLTYEDHGAPFAGH 1553
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
730 ANG-----EKGEVGPFPAGSAG---ARGAPGERGETGPPGTSGIA---GPPGAD- 773
QY 1554 LPRGSPVTMREPTPLQEGSLSSSKASQDRKLTSTPREIAKSPHSTVPEHHHPHPSPEYH 1613
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db 774 ---GQPCAKGQCEAGQKGD-----AGAPGQPGSAGAPQGP--- 808
QY 1614 LLRGVGVDLRSHIPLAFDPTSIPIRGIPLDAAAYVLRHLAPNPTIPLYPPYLIRGY 1673
Db 809 --TGVTPKGARG---AQCP---PGATGPPGAGRVGPPGSNGNPG-----PP---GP 850
QY 1674 PDAALLENQTIINDYITSOQMHNTATAMAQADMLRGLSPRESSLALNYAAGP----- 1728
Db 851 PGPSGKGDPK-----GARGD---SGPPGRAGEPGLQGPAGPPGKEG 888
QY 1729 -----RGIIDL-----SQVPHL---PVLVPPPTGTTATAMDRL 1758
Db 889 EPDGDGPGSAGBPPGQGLAGQIGVLPQORGERGFPGLPGSPGPGQAGPAGSGDR- 947
QY 1759 AYLPTAPQPPSSRHSPLSPGPGTHLTPTTSSSRERDRDRDREREKSILTST 1818
Db 948 -----GPPGVPVPPGLT----- 959
QY 1819 TTVEHAPIWRPGTEQSGSGSGSGSGSSSRPASHSHAHQHSPISPTODALQORPSVL 1878
Db 960 -----GPAGEPGRGSPGADGPPGRDGA----- 983
QY 1879 HNTGKGIITAVEPSKPTVLRTSTSSPVRPAATFFPATHCPLG-----GTLDG 1927
Db 984 ---GVKG-----DRGETGAVGAPGAPGPPSPGAGTCKQKQDRGEAGAQP 1027
QY 1928 VYPTLMEPVLKPKEAPRVARPERPRADTGH-----FLAKPPARSGL 1969
Db 1028 MGFS-----GPAGARGIQCPQPRGDKGAGBGERGLKXRGFTCLQGLPFPSPSGD 1081
QY 1970 EPASSPSKGSSEPLVPPVPSGHATIARTPAKNLAPHASPPDPAPPASDPHREKTQSK 2029
Db 1082 QGASGPAGPSGPR-----GPPGVPGPS----- 1103
QY 2030 PFSIQLELRLSLGHGSSYSPGVEPVSVPSSPLTHDKLPHLBEELDKSHLEGELRPK 2089
Db 1104 -----GKDGANGIPGIPGPPGRSGRSETGPAGPPGN-----PG 1137
QY 2090 QPQPVKLGGEAAHLPHLRPLPESQSSPLL-----QTAPGVKGHORVV-----TLAQHI 2139
Db 1138 PPGPPGPPGICMDSAPAGLGPKEKDPDPLQYWRADQAAGLQHQDAEVDTLKSNNQI 1197
QY 2140 SEVITODYTRHHPQOLSAPLAPLYSPGASCPLVLDLRRP---PSDLYLPPPDHGAPARG 2197
Db 1198 ESIRSPGSKNPAR-----TCRDLKLCHPEWKSQDVIWDPNQCTILDAM 1242
QY 2198 P---HSEGGKSPPEPKTSV-----LGG-----GEGDIEPVSP 2227
Db 1243 KVFENMETGETCVYPNPANVPKKNWSSKSKEKKHIWFGETINGGFHFSYGDNDLAPNTA 1302
QY 2228 PEGWTEPHRSASVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFPSKLTESNAGMVKSK 2287
Db 1303 NVQMT-----FLRLSTEGSON-----ITHCKNSIAYLDEAA 1335
QY 2288 QEINKKLNTHNRNEPEYNISQPGTEIFNMPAIT-----GTGLMYRSQ 2330
Db 1336 GNLKALLIQSDNVE---IRAEGNSRFTYTALDKGCTKHTGKWKGTVIEVRSQ 1386

RESULT 85

US-09-500-811-20
; Sequence 20, Application US/09500811
; Patent No. 6323314
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC

STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
US-09-500-811-20

Query Match 2.5%; Score 330.5; DB 4; Length 1418;
Best Local Similarity 20.4%; Pred. No. 1.2e-10;
Matches 378; Conservative 117; Mismatches 631; Indels 727; Gaps 86;

QY 721 AEALHAGNEV---PRGECSGATVNNSSDTSISPSHTEAAK-----DTGQNG-P 767
Db 18 AAVLCQGOQVROFGPKQKQEGEDIKDIVGPKPPQGPAGEQGRGDRDKGEGAP 77
QY 768 KP-----PATIGADGP--PPGPPTTP-----RRTSRAP 794
Db 78 GPRGRDGEPTLGNPGPPGPPGPPGLGNGFAAQWAGGFDEKAGAQQLGVMGPM 137
QY 795 EPTPASEATGATP-----PPAPSPSAPPPVVPKKEEETAAAPVVEGEBQKPPAA 848
Db 138 GPRGPPGAPAGPQGFQGNPGEFGEFVSGPMGR-----GPP---GPPGKPG-- 183
QY 849 EELAVDTKAEVPKSECTEAESEKPAKXDAEAAEATASGALKAEKKGSGRATTAKS 908
Db 184 -----DDGEAGKPKA-----GERGPPQPGARFPGT-PCLPGVKGHRGYPGLDGAKE 232
QY 909 SGAPQDSSSATCSADEVDEAGDKNRLSPRLTTPGDRANASPKPLDLKQLKQ 968
Db 233 AGAP-----GVKGE-----SGSPGNGSP-GPMGPRGLPG 261
QY 969 RAAAIPIQVTKVHEPPREDAAPTKPAPPAPPPQNLPESDAPQPGSS----- 1018
Db 262 ERGRTGPAGAAGAR---GNDGQPGAPGPPGPPGPPGPPGAPGAKGEAGPTCARGPEG 318
QY 1019 ---PRGKSRPAPPAKAEFAAAQKLPDGPCCWTSGLPFPVPPREVIVKSPHAPDPSAF 1075
Db 319 AQGPRGEPGTPGSPG-----PAGASGNPG-----TDGIP-----GAKGSAGAPGIA-- 359
QY 1076 SYAPPCHPLGLHDTARVLPRLPPTISNPPLISSAKHPSVLERQIGAISQGSMSVLHV 1135
Db 360 --GAPGPPGPRG-----PPD-----PQG----- 375

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
US-09-548-608-20

Query Match 2.5%; Score 330.5; DB 4; Length 1418;
Best Local Similarity 20.4%; Pred. No. 1.2e-10;
Matches 378; Conservative 117; Mismatches 631; Indels 727; Gaps 86;

421 KRG-ARGE-PGGVGPPIGPFGERCAPGNRGFPQDGLAGPKGAP-----GERG 465
1252 PSRL-----DRGR--EDSLPKGHVYVEGKKHVLVSYEGGMSVTQCKEDGRSSGPP 1301
466 PSGLAGPKGANGDPGRPGEPGLPGARGL-TGRPGDA-GPQKVGPSGAPGEDGR--PGPP 521
1302 HETAA-----PKTYDMMEGRVRA-----ISSASIEGLMGR-----AIPPER 1339
522 GPQARGQPGVMGFPQPKGA---NGEPKAGEKGLPGAPGLRGLFGKDGEGTGAEGPPGP 577
1340 HSPHLKKEQHIRG-SITQIPRSYVEAQEDYLRLREAKLLKREGTPPP-----PSSDL 1393
578 AGPAGERGEGGAPGPGFQGLP-----GPPGPPEGKPKDQGV 616
1394 T-BAYKTQALGPL-----KLKPAHEGLVATVKEAGRSIHIEIPREELRHTPELAPR 1444
617 PGEAGAPGLVGRGERGFPGERGSPGAQGL---QGRGLPGTGTGDKPGKASGAPGP 671
1445 PLKEGSIOTGTPLYDTGASTTGSKKHD-----VRSLLSGR-----TFPPVHLDVM 1493
672 GAQPPGLQMP--GERGAAGIAGKDRGDVGEKGPAGKDGGRGUTGPIGPPGAP 729
1494 ADARALERACYBESLKSRTASSGSIARGAPVIVPELGPQRQSPPLTYEDHGAPFAGH 1553
730 ANG-----EKGEVGPFGPAGSAG---ARGAPGERGETGPPGTSIA---GPPGAD- 773
1554 LPRGSPVTWREPTPLQEGSLSSSKASQDRKLTSTPREIAKSPHSTVPEHHPHIPSYEH 1613
774 ---GQFAGKEQGEAGKGD-----AGAPGQPGSGAPGQGP--- 808
1614 LLRGVSGVDLYRSHIPLAPDPTSIPIPLDAAAAYVPLHPLAPNPTYPHLYPPYLIRGY 1673
809 --TGTGPKARG---AOGP--PGATGPGAAGRVGPPGNGNGP-----PP-----GP 850
1674 PTAALENRQTIINDYITSQQMHNTATAMAQADMLRGLSPRESSIALNYAAGP----- 1728
851 PGPSGKDGPK-----GARGD--SGPPGRAGEPGLQGPAGPGEKG 888
1729 -----RGIIDL-----SQVPHL--PVLVPTPTGPTATMDRL 1758
889 EPGDDPGSAEGPPGPGLAGQRIIVLPGQGERGFGLPGPSGEPGQGGAPGASGD- 947
1759 AYLPTAPOPFSSRHSSPLSPGCPHLLTKPTTTSSSERDRDRDRDREREKSILTST 1818
948 -----GPPGVPPGLT----- 959
1819 TTVEHAPIWRPQTEOSSSGSSGGGGSSRRPASHAHQHSPISPRTQDALQORPSVL 1878
960 -----GPAGEPREGSPGADGPPGRDGA-- 983
1879 HNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPTHCPILG-----GTLDG 1927
984 ---GVKG-----DRGETGAVGAPAGPPGSPGAPGTGKQDGRGAGAQP 1027
1928 VYPTLMEPVLVPKEAPRVARPERPRADTGAH-----FLAKPPARSGL 1969
1028 MGPS-----GPAGARGIQPGQPGDKGEAGEPGERGLKGRGFTGLQGLPGPQPSGD 1081
1970 EPASSPSKSEPRPLVPPVSGHATTARTAKNLAPHASPDPPAPPASASDPHREKTSK 2029
1082 QGASGAPGPGSPR-----GPPGPVGPS----- 1103
2030 PFSIQELELRSLGYHGSYSPEGVPSVSPSLTHDKGLPKHLELDKSHLEGELRPK 2089
1104 -----GKQANGIPGIPGPPGRSGGTGAPGPCN-----PG 1137
2090 QPGPVKLGAEHLPLRPSPSSPFL-----QTAPGVKGRVV-----TLAQHI 2139
1138 PPGPPGPGDMSAFAGLGPREGPDPLQVYMRADQAAGLGRQDAEVDATLKLNNQI 1197
2140 SEVITQDTRHHHPQOLSAPLPAPLYSFFGASCVPDLRRP--PSDLYLPPPHGAPARG 2197

Db 1198 ESTRPEGRKPNAR-----TCRDCLKLCHPEWKSQGYWIDPNOCCTLDAM 1242
Qy 2198 P---HSEGGKRSPEPNKTSV-----LGQ-----GEGDIEPVSP 2227
Db 1243 KVCNMTGETCVYPNANVPKKNWSSKSEKKHIWFGETINGGPHFSYGDNDLAPNTA 1302
Qy 2228 PEGWTEPCHRSAYVPLLYRDGQTEPSRGMKSPGNTSQPPAFFSKLTSNANWKSXK 2287
Db 1303 NVQMT-----FLRLSTEGSQN-----ITYHCKNSIAYLDEAA 1335
Qy 2288 QEINKKLTHNRNEPEYNIQSQGTIEFNMPAIT-----GTGLMTYRSQ 2330
Db 1336 GNLKXALLIOGSDNVE--IRAEGNSRFTYALKDGGCTKHTGKWKTVIERSQ 1386

RESULT 88
US-09-252-991A-29427
; Sequence 29427, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29427
; LENGTH: 1476
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29427

Query Match 2.5%; Score 329; DB 4; Length 1476;
Best Local Similarity 20.4%; Pred. No. 1.6e-10;
Matches 333; Conservative 147; Mismatches 557; Indels 596; Gaps 78;

Qy 536 PEVENDKEDLLKKTDDTSGEDNDEKEAVASKRKTAN-----SQRRKGRIT-----RS 585
Db 160 PFVEGRRRLRRE-AGETRODDTDE-----KGKCAHRHSGPETQGTDTLTTPAPRS 212
Qy 586 MANEANSSEAITP-QQSAELASMLNESSRWTEEMETAKGLLEHGRNWSAIARMVGSK 644
Db 213 NPSRSDCHRGDPFCTNDSRVAAGLDPPP--GADELRSYRR--CEHG-----255
Qy 645 TVSQCKNFYFNKKRQNLDEILOQHKLMKEKERNARRKKKAPAAA--SEEAAPPPVVEDE 703
Db 256 ----C-----IRTHERPFAATLQSPCLRFSSKKPSPTPDAD 290
Qy 704 EMASGVSGNEEWEAEALHASGNEVPRGCSGPATVNSDDTSPSPHTEAAKDTG 763
Db 291 RLRLA-----DPRRGHRTSR-----SAHLAAAGTRA 318
Qy 764 QNGPKPATLADGPPPPPTPRRTSRAPTEPTPASEATGATPPPPSPSPSAPPVVP 823
Db 319 GTLCRDPLGAPGSGRHVPGGRPLRPPPLRPVAFVHAAPVRPLRHHPP--PGALLP 376
Qy 824 KEEKEBETAAP-----PVEEGEEQKPPAAE-----ELAVDTGKABEVPKSECTEEA--- 870
Db 377 GTDARRTPAVPALRGKPGCGRAGHRLPRRADLRPLSATALRELRCQPAAGGAEPVHR 436
Qy 871 EEPGAKGDAEAEATAEGALK-----AEKKGSGGPAATKAGSGAPQDSDSATC----- 921
Db 437 EPRPARSRTPLQPGGGLSLHPCGAVAGQDARLQRLRALLRHQHPGPDREIPLCRRAH 496
Qy 922 -----SADEVEAEGDKNRLLSRPPSLITPTGDPANASPKPLDLKQKORAAAI 974
Db 497 ROHRRQAADAL-----GQRTQ--LSRRPGQLRRAPGHRAH-----LPQLGAAGV 539

Qy 975 PIQVTKVHEP-----PREDAAPTKPAP-PAP-----PPQNLOPE 1008
Db 540 GAGLRGRHGRWVGLVRRRLPAGRRGTRRQGRTRRPPGPGPAGAGADDRPPPAFLLSG 599
Qy 1009 SDAPOQPGSSPRCKSRSPAP-----PADKEAFABEAQKLP 1044
Db 600 AARPRRAGDDDRPPAGDPDGRHRGAIVTCGAGTEAGVPRPPQPADGATAADQOGRDPG 659
Qy 1045 DPPCWTSGLPFPVPPREVIKASPHADPS--AFSYAPPG-----HPLPLGLHDTARPVL 1096
Db 660 SHP-----PGRDAREATVR-PPSPRAGQYHPPARVAGKRHL-----LAETRRPGL 705
Qy 1097 PRP-----PTISNPPPLISSAKHP--SVLERQIGAIOSQMSVOLHVPVSEHAK---AP 1144
Db 706 RRPARADRRTPADFDLDLTGLQLHFVRTYAERQPGA---GADRQ-HRPALRHQRQOAG 761
Qy 1145 VG---PVTMGLPLPMPKPLAPFSQKQEQLSPRGOAG-----PPESLGVPTQAEASVLR 1196
Db 762 VGLHROATGAGQLPGDRRADPPRLWRHERRAAQGGSGAARFHPPLGHRLPGRQP-----R 817
Qy 1197 GTALGSPVPGGSITKGIPTRVPSDSALTIVRGSITHGTTPADVLYKGTITRIIGEDSPSRLD 1256
Db 818 PRSFRDAPGG-----HG-----TALFGQPLRELLH 842
Qy 1257 RGRE---DSLPGKHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETA-APKRTYD 1312
Db 843 RRRAAHLQQLPQGR-----QRPDPADAAGSPAR---869
Qy 1313 MMEGRVGRAISSASIEGLMCRATIPPERHSPHLKEQHIIHRSITQGITPRSVVQAQEDYLR 1372
Db 870 -----IDQPALRAPAAPDPFP-RYLPER-REQAVAGRRQGPAP-----R 907
Qy 1373 REAKLLKREGTPPPPPSRDLTEAYKTQALGPKLKPAPHEGLVATVKEAGRSIHEIPREE 1432
Db 908 RLPRPFRQCKPGLPAP-----LLG-----QVRQ 933
Qy 1433 LRHTP-ELPLAPRLKEGSITQGTPLKYDTGASTTCKKHVDVRLSGISGRTPTPPVHPLD 1491
Db 934 RQAPGDLPRRPASL-AGAAGRDPLPAATG-----RPGELQRL-----PPRTAPRQP-D 982
Qy 1492 VMADARALERACVYESISKSPG-----TASSSGSITARGA-----1526
Db 983 RQARRRAVRLRGQVQVQPPGRLRRPRAPAGAMAARLSAEAAAGDLRRGGGQRRRAQGG 1042
Qy 1527 ---PVTVPRLGKPRQSPLYTIEDHCAFP-AGHLPRGSPVTMREPTPRIQESLSSSKASQD 1582
Db 1043 LRLAVQVAQERPROA-----HPHPAGGGGLR-----PAPAMEETEL--SLRSPG 1086
Qy 1583 RKLSTSTPREIAKSP-----HSTVPEHHPHPI 1608
Db 1087 ALLRHFRPGQLRRPPGGAGRTDGDHRQWRRAHADPAPGAPRLRPGYALRDALRPGSHPRP- 1145
Qy 1609 SPYEHLLRGVGVLDLYRSHIPLAFDPTISPRGIPLDAAAAYLPRHLAPN-----1658
Db 1146 -----AGDDLGRHDPA---QRAVPGGRRRRRAAP---ARHLQPSGRRATGGRQ 1189
Qy 1659 -----PTYPH-----LYPPYLIRGYPDTAALENQTIINDYITS 1692
Db 1190 DRHRQPPADLQRRRPAQPEGTEPHRFLHRLHPAALR-YPH--RLRRQR-----VEP 1241
Qy 1693 QQMHNTATAMAQADMLRGLSPRESSLALNYAAGPRGIIDLQVPHLPVLPPPTPTPA 1752
Db 1242 VQVHLGPASAGTQ-----GHGTAPOGL-----PR-PTHRHPLPGTVV 1277
Qy 1753 TAMDR--LAYLTPAQPFSSRSHSSPLSPGTPHLYKPTTSSSERDRDRDRDRER 1810
Db 1278 AATDRPFAVQRTQYQAGRSSRSRPMRVSPKSFSPSEWHSG-----C 1322
Qy 1811 EKSILTS-----TTTVEHAPIW-----RPGTEQSSGSGSGSGSGSGSSRRPASHS 1855
Db 1323 SSSVATISRAACDTTSTWECCAAMPTRPRAGSRSGGCELVSGLSTSSAGRGONRAIHS 1382
Qy 1856 HAHQHSPIGPRTQDALQORPVLHNTGMK-----GIITAVEPSKPTV 1897

Db 1383 R-YRRVPSDSSAVRSRRCGCSISTSKRPLGLSMCRRLPKCKASSTASSAAASPISRMV 1441
QY 1898 LRSTSTSPVRPA 1910
Db 1442 CRAARSAPSAPS 1454
RESULT 89
US-09-010-999-1
; Sequence 1, Application US/09010999
; Patent No. 6132976
; GENERAL INFORMATION:
; APPLICANT: Poole, Anthony R.
; APPLICANT: Hollander, Anthony P.
; APPLICANT: Billingshurst, R. C.
; TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
; TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,999
; FILING DATE: 22-JAN-1998
; CLASSIFICATION: 4335
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,501
; FILING DATE: 17-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/984,123
; FILING DATE: 04-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 032931/0212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human Type II Collagen
US-09-010-999-1
Query Match 2.5%; Score 328; DB 3; Length 1418;
Best Local Similarity 22.2%; Pred. No. 1.7e-10;
Matches 327; Conservative 85; Mismatches 557; Indels 502; Gaps 77;
QY 721 AEALHAGNEV-----PRGCSGATVNNSSDTESIPSPHTEAAK-----DTQNG-P 767
Db 18 AAVLRCCQDVDPGPKGKEGPDLDIVGPKGPGQPGAPGQGRGDRGDKGEGAP 77
QY 768 KP-----PATLGADGP--PPGPPTPP-----RRTSRAP 794
Db 78 GPRGRDGEFTLGNPFGPPGPPGPPGLGGNFAAQWAGGFDEKAGCAQLGVNQGMGM 137
QY 795 EPTPASEATGATP-----PPAPPSAPPVPPVVKKEEETAAAPVVEEGEEKPPAA 848

Db 138 GFRGPGPAGAPGQFQGNRGEPEGPGVSGPMGPR-----GPP-----GPPGKPG-- 183
QY 849 ELAVDTGKAESPVKSECTEAEAGPAKGDAAEAATAEAGAKAEKKGGSGGSRATTAKS 908
Db 184 -----DDGEAGKPGKA-----GERGPPGQARGFPGT-PGLPGVKGHRGYPGLDCAKGE 232
QY 909 SGAPQSDSSATCSADEVDEAEGDKNRLLSRPPLSLTFTGDPANASQKPLDLKQLKQ 968
Db 233 AGAP-----GVKGE-----SGSPGNGSP-GPMGPRGLPG 261
QY 969 RAAAIPIQVTKVHEPPREDAAFTKAPPAPPPQNLQPESDAPQPPGSS----- 1018
Db 262 ERGRTCPAGAAGAR---GNDGQFGPAGPFGVPGAGGPGFPGAGKAGAGTARGPEG 318
QY 1019 ----PRKSRSPAPPADKEAFAAOKLPDPPPCWTSGLPFPVPPREVIVKASPHAPPSAF 1075
Db 319 AQCPRGEPGTGSPG---PAGASGNPG---TDGIP-----GAKGSAGAPGIA-- 359
QY 1076 SYAPPGHPLPLGLHDTARVLPVPRPTISNPPPLISSAKHPSVLERIGAISQMSVOLHV 1135
Db 360 --GAPFGPGRG-----PPD-----POG----- 375
QY 1136 PYSEHAKAPVGV-TMGLPLPMDPKLAPFSGVKOBQLSPRGOAGPPELSLGVPTAGEASV 1194
Db 376 -----ATGFLGPKGTGKP-----GIAGFKGEQ-CPKGEPPAGPQAGPAGGEG 420
QY 1195 LRGTALGVPGSGITKGIPISTR-VPSDSAITVRSIT--HGTPADVLYKGTITRIIGDS 1251
Db 421 KRG-ARGE-PGSGVPTGPPGERGAPGNRGFPQDGLAGPKGAP-----GERG 465
QY 1252 PSRL-----DRGR--EDSLPKGHVIEGKKHVLSEGGMSVTQCSKEDGSSSGSP 1301
Db 466 PSGLAGPKANGDPGRPGEPGLPGARGL--TGRPGA-GPQGVKVGSGAPGEDGR--PGPP 521
QY 1302 HETAA-----PKRTYDMEGRVGRA-----ISSASIEGLMGR-----AIPPR 1339
Db 522 GPQARGQPGVMGFPCKGA---NGEPKAGEKGLPGAPGLRGLPGKDGETCAEGPPGP 577
QY 1340 HSPHLKEQHIRG-SITOGIPRSVVEAQEDYLRREKLLKREGTTPPP-----PPSRL 1393
Db 578 AGPAGERGQAGPSPGFGQLP-----GPPGPGEGKPGDQGV 616
QY 1394 T-EAVKTOALGPL-----KLKPAEGLVATVKEAGRSIHEIPEELRHTPELPLAPR 1444
Db 617 PGEAGAPLVGPRGERGPPGERGSGQAQL-----QGPRGLPGTGTGPKKASGAPGP 671
QY 1445 PLKEGSIQTGTPLKYDTGASTTGSKKHD-----VRSILIGSPGR-----TFPPVHPLDYM 1493
Db 672 GAQGGPGLQGMF--GERGAAGIAGPKGDRGVGKGEKGPAGKDGGRGLTGFIPGPPAG 729
QY 1494 ADARALERACYEESLKSRPGTASSSGSIARGAPVIVPELGHKPROSPLTYEDHGAFFAGH 1553
Db 730 ANG-----EKGEVGPFPAGSAG---ARGAPGERGTGPPGTSIA-----GPPGAD- 773
QY 1554 LPRGSPVTWREPTPLQEGSLSSSKASQDRKLTSTPREIAKSPHSTVPEHHPHSPYEH 1613
Db 774 ---GQPGAKGEQGEAGQKD-----AGAPGQGSAGAPGQGP----- 808
QY 1614 LLRGVGVDLYRSHIPLAFDPTSI PRGIPLDAAAAYLLPRHLAPNPTYPHLYPPYLIRGY 1673
Db 809 --TGVTGPKARG---AQGP---PGATGFGAAGRVGPPGSGNNGP-----PP---GP 850
QY 1674 PTAALENRQTIINDYIYSQMHNTATAMAQRADMLRGLSPRESSLAINAAGP----- 1728
Db 851 PGFSKDGPK-----GARGD---SGPPGRAGEPLGQSPAGPPEKG 888
QY 1729 -----RGIIDL-----SOVPHL---PVLVPTPTGPTATMDRL 1758
Db 889 EPGDDGPGSAEGPPGQGLAGQGVGLPGQGERGFGCLPGPSPGEPGQGGAPGASGR- 947
QY 1759 AVLPTAPOFFSSRHSSSPLSPGPHLTKPTTTSSSRERDRDRDREREKESILST 1818

1782 PTHLTPTTSSSERDRDRDR-----DREKESILTSTTVE-----1822
1079 PTH-AQGLVSSATQYGAHQTHAMVACPKLPYNKETSFPYFAISTGSLAQYAHFNA 1137
1823 ----HAPIWPGTEQSGSGSGSGSGSSRRPASHSHAHQHSPISPRTDALQORPSVL 1878
1138 TLHPHTPHQP-SATPTGQOOSQHGGSHAPSPVQH---HQHQAALHLASPOQSAIY 1193
1879 HNTGMKGIIITAVPSPKPTVLURSTSTSP-----VRPAATPPP-ATHC 1919
1194 H-----AGLAPTPSMTPASNTQSPQSFPAQAQVPTIHPSHVQPAYTNPMAHV 1245
1920 PLGGTLDGV---YPTLWBPVLLPKEAPRVARPERPRADTGHAFIAKPPARSGLEPASSPS 1976
1246 POAHVQSGMVPSHTAHAPMLMTTP-----PGPQAAL-----AQALQIPVST 1292
1977 KGSEPRPLVPPVSGH 1991
1293 TAHFPYNTHPVQAH 1307

RESULT 92
US-09-707-919A-19
; Sequence 19, Application US/09707919A
; Patent No. 6623927
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: Method for detection of human spinocerebellar ataxia 2
; TITLE OF INVENTION: gene variants
; FILE REFERENCE: US 443
; CURRENT APPLICATION NUMBER: US/09/707,919A
; CURRENT FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 19
; LENGTH: 1312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-707-919A-19

Query Match 2.5%; Score 325.5; DB 4; Length 1312;
Best Local Similarity 19.6%; Pred. No. 2.2e-10;
Matches 320; Conservative 166; Mismatches 516; Indels 631; Gaps 75;

492 KSQQQQQQQQQQQQQQQQQQQQPMSRQBEKDEKEKEKEKEKEKEPEVENDKEDLKEKTD 551
169 QQQQQQQQQQQQQQQQQQQQQPPAAANVRKPGGGGLLASPAAPSP-----213
552 DTSGEDNDEKAVASKGRKTANSQGRKGRITRSMANEANSEEAITPQQAELASMEELNE 611
214 --SSSSVSSSSATAPSSVVAATSGGRPG---LGRGRNSKGL-PQSTISF-----258
612 SSRWTEEMETAKGELLEGRNWSAIARMVGSKTVSQCKN--FYFNKKEQNLEILQOH 669
259 -----DGIYANRVRVHILTSVVGSKCEVQVKGIGY-----EGVEKTY 296
670 KLMKEKERNARRKKKAPAAASEAAPPPVVEDEMEASGVSGNEEBMEVEAEALHASGN 729
297 SPKCDLVDAHEK-----STESS-----SGPKREIMESILFKCSDF 334
730 EVPRGECGPATVNNSDTESIPSPHTEAAKDTGQNGKPKPATLGADGPPPGPTPPRRT 789
335 VVQFKDMDSSYAKRDAFTDAIS-----AKVNGEHEK-----368
790 SRAPIETPASEATGATPPPPAPPSPAPPVVPVKEKEKEEETAAAPPVEG-----840
369 ---DLEPWDAGELTA-----NEELELENDVNSGWDPNDFRY 403
841 EEQKPPAAEELAVDTGKAEPVKSECTEAEEGPAKGD-AEAAEATAEGALKAKEKEGG 899
404 NEENYGVVSYDSSLSTYTPLEKDNSEEFLEKREARANQAELEESSAQ---YKRAVALEN 461
900 SGRATTAKSGAPQDSSSATCSADEVDEAGGD-----KNRLISP--RPSLLTPTGDPRA 953

462 DRSSEEEKYTAQVRNS-----SREGHHSINTRENKYIPPGQRNREVISMSSGRQ 510
954 NASPQKPLDLKQLKQRAAAIPIQVTKVHEPREDAATKPAAPPAPPPONLQSPESDAPQ 1013
511 NS-----PRMGQPGS-----520
1014 QGSSSPRGKSRSPAPPADKEAFAAEAKLPGDPCCWTSGLPFP-----VPP 1059
521 --GSMB---SRSTSHTSDFNPNSGSDQRVVNGGVWPSPCPSPSSRPPSRYSQSGPNSLPP 575
1060 REVIKASHPAPPSASYPAGHPPLGLGLDHTARVLPRLPPTISNP--PPLIS--SAKHP- 1115
576 RAATPTPRPSRPSRPS--RPPSHP---SAHGSAPVSTMPKRMSSGPPRMSKPAQHPR 631
1116 -SVLERIQIGAISQCMGSQLHVPYSEHAKAPV-----GVTWGLPLPMDPKKLAPF 1164
632 NHRVSAGRSISGLFVSHNPPSEATPPVARTSPSGGTWSSVSGVP--RLSPKTHPR 690
1165 SGVKQEQOL--SPRG-----QAG--PPESLGVPTAQEASVLRGTALGSPGGSITKGPS 1214
691 S-PRQNSIGNTPSGPVLASPGAGIIPTEAVAMP-----IPAASPTPASPA 734
1215 TRVPDSAITYRCSITHGTTPADVLYKGTITRIIGEDSPSLDRGREDLSLPGHVIYEGKK 1274
735 ----SNRAV-----TPS-----SEAKOSRLQDORONS--PAG-----760
1275 GHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRRAISSASIEGLMRA 1334
761 -----NKENIK-----PNETSP-----SFSKAENKGI-SPV 785
1335 IPPERHSPHLKE--QHIRGSIITQIGIPRSYVEAQEDYLRREAKLLKREGTPPPPPSRDL 1393
786 VSEHRKQIDDLKKFNDRLQ-----PSSTSEMDQLLNK-----NREG-----EKSRDL 830
1394 TEAYKTQALGPLKKAHEGLVATVKEAGRSIHEIPREELRHTPELPAPRLKEGSIQ 1453
831 IKD-----KIEPS-----AK 840
1454 GTPLKYDTGASTGSKKHVRSLSIGSGRTFPVPHPLDVMDADARALERACYEESLSRPG 1513
841 DSFIENSSNCTSGSKPN-----859
1514 TASSSGSIARGAPVIVPELGKPRQSLTYEDHGAPFAGHLPRGSPVTMR-----EPTPR 1568
860 -----SPSISPSI-----LSNTEH-----KRGPEVTSQGVQVTSPPACK 892
1569 LQEGSLSSSK--ASQDRKLTSTPREIAKSPHS--TVPEHHPHPISPYEHLRGLGSGVDLYR 1625
893 QEXDDKEEKDAAEQVRKSTLNPNAKFENRSPSQPKPSTTPTSPRPAQSPSPSMVGHQ 952
1626 SHIPLAFDPTSI PRGIPLDAAAAYLPRHLAPNTPVPHLYPPYLLIRGYDPTAALENR--- 1682
953 -----PT-----PVYTOPVCFAPNMMYFVPSFGVQLYPI---PMTFPMVNOAKT 995
1683 -QTIINDYITSQMHNTATAMAQADMLRGLSPRESSLALNVAAGPRGIIIDLSQVPHLP 1741
996 YRAVPMNQORQDQHQA-----MMHPAS-----AAGP-----P 1025
1742 VLVPTPTGPTATMDRLAYLPTAQOPSSR-----HSSSPISLPGG-----1781
1026 IAAATP-----PAYSTQVAY---SPQOPFNQPLVQHVPHYSQHPHYVSVIQGNARMAP 1078
1782 PTHLTPTTSSSERDRDRDR-----DREKESILTSTTVE-----1822
1079 PTH-AQGLVSSATQYGAHQTHAMVACPKLPYNKETSFPYFAISTGSLAQYAHFNA 1137
1823 ----HAPIWPGTEQSGSGSGSGSGSGSSRRPASHSHAHQHSPISPRTDALQORPSVL 1878
1138 TLHPHTPHQP-SATPTGQOOSQHGGSHAPSPVQH---HQHQAALHLASPOQSAIY 1193
1879 HNTGMKGIIITAVPSPKPTVLURSTSTSP-----VRPAATPPP-ATHC 1919

STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,443
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/049,477
FILING DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 235/055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1274 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-095-443-2

Query Match 2.5%; Score 324.5; DB 4; Length 1274;
Best Local Similarity 21.3%; Pred. No. 2.4e-10;
Matches 326; Conservative 172; Mismatches 551; Indels 485; Gaps 79;

267 HENIKINQAMKRLILYFKRNRHAKQKFCQRYDQLMLEALEKVKVERIENPRRAKE 326
4 HEASSLYSEKAKL-----REMAKIEDKNEV---LDQFMDSMQLDPEIVDN----- 48
327 SKRYEYKQFPPIRQ-----RELQRMQSRVQQRSGISMSAARSEHVSEI 375
49 ---LDAYSHIPPQMEKCAALSVRPDTVRNLVQSMQV-----LSGVFTDVEASLKDI 97
376 IDGLSEQENLEKQMLAVIPPLYDADQRIKFINWGLMADPMKYKDRQVWVWSE- 434
98 RDLLEDELLEQKFOEA-----VGAGAITSITKA-ELAEVRREWAKY 139
435 ---QEKETFREKFMQ-----HPKNFGLIASFLERKTV-----ECVLYYLTKN 476
140 MEVHEKASFTNSLHRAMNLHVGNLLSGPLQDVRAALPTPALSPEDKAVL----- 191
477 ENYKSLVRRYRRGKSGQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 536
192 QNLKILAKVQENR---DQVSLQQLRELKQDDITASLVTTHDSEMKKLFEEQLK-- 245
537 EVENDKEDLLKKTDDTSGEDNDEKAVASKGR-----KTANSQGRKGRITSMANEAN 591
246 ---KYDQKLVYLE-----QNLAAQDVRVLCALTEANVQYAAVRVSLDLDKQWN 290
592 SE-EAITPQOSABLASMELNESSRWTEEMETAKKGLLEHGRNWSAIAIRVMSKTVSOCK 650
291 STLQTLVASVEAYEDLMKKSQEGRDFVADLESKVAALLE-----RTQSTCQ 336
651 NFYFNKKNQNLDEILQQHKLKWKERNARKKKKAPAAASEEAPPPVVVEDEMEASGV 710
337 -----AREAAQQLDRE-----LKKKPPPPPTAPKPLPRRESEAVEAG-- 377
711 SGNEEEMVEAEALHAGSNEVPRGEGSGP-----ATVNNSDTESIPSPHTEAKDTGQ-- 764
378 -----DPPEELRSL-----PPDMVAGPLPLDTFLGSAITPLHFPSPFPSS---TGQGP 422

RESULT 97

US-08-728-323A-2

; Sequence 2, Application US/08728323A

; Patent No. 5948676

GENERAL INFORMATION:
 APPLICANT: Chang, Yuan
 APPLICANT: Bohenzky, Roy A.
 APPLICANT: Russo, James J.
 APPLICANT: Edelman, Isidore S.
 APPLICANT: Moore, Patrick S.
 TITLE OF INVENTION: Immediate Early Protein From Kaposi's
 TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
 TITLE OF INVENTION: Encoding Same And Uses Thereof
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/728,323A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0525
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1162 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-728-323A-2

Query Match 2.5%; Score 324; DB 2; Length 1162;
 Best Local Similarity 19.3%; Pred. No. 2.3e-10;
 Matches 135; Conservative 135; Mismatches 293; Indels 138; Gaps 18;

QY 146 EPVSP-----SPHTDPELEVPRLSKEELIONMDRVREITMVEQQLSKKKQ 197
 DB 461 EPLQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQ 520
 QY 198 QLEEEAAKPEPEKPVSPPIESKHSLSVLIYDNRKKAEEAHRILEGLGPQVELPLY 257
 DB 521 QQ--EPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQ 571
 QY 258 NQSDTRYHENIKINQAMRKLLIFKRNHARKQWKQFCORYDQLMALKKVERIE 317
 DB 572 REPQREP-----QQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQ 612
 QY 318 NNPRRAKESKVREYKOPPEIRKQRELQERMQSRVQSGSLMSAARSEHVSIIID 377
 DB 613 DEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDE 669
 QY 378 GLSEQENLEKQMLQAVIPMLYDADQORIKFINMGLMADPMKYKDRQVMNWSQEK 437
 DB 701 EQQDEQQDEQEQE-----QQDEQ-----QDEQQDEQQDEQQDEQQDE 700
 QY 438 ETPREKFMQHPKNGFLIASFLERKTVAECLVLYLTKNENYKSLVRRSRRRGKSGQQQ 497
 DB 701 EQQDEQQDEQEQE-----QQDEQ-----QDEQQDEQQDEQQDEQQDE 737
 QY 498 QQQQQQQQQQQQQMPRSSQEQEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKE 556
 DB 738 QDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDE 795

QY 557 DNDEKAVASKGRKKTANSQGRKRITRSMANSEEAITPOOSAEALSMELNERRWT 616
 DB 796 ELEEQEQELEEQELEEQEQE-----LEEQEQELEEQELEEQELEEQELEEQEQEV 851
 QY 617 EEMETAKKGLLEHGRNWSAIAARMVGSKTVSQCKNFYFNKKQNLDEILQQHKLKMEKE 676
 DB 852 EEQEQEQEQELEEQE-----VEEQEQEQEQEQEQEQEQEQEQEQEQEQEQEQEQEV 895
 QY 677 RNARRKKKAPAAASBEAAPPVVVEDEMEASGVSGNEEEMVEEAALHASGNEVPRGEC 736
 DB 896 ----EEQEQELEVEEQEQEQELEVEEQEQEQEQEQEQEQEQEQEQEQEQEQEQEQ 950
 QY 737 SGPATVNNSSDTESIPSPHTE-AAKDTGQNGPKPATLGDAGPPGPPTPRTSRAPIE 795
 DB 951 DYP-----VVSTHEQIASSPPGNDTPD-----DDPQPGFSREYRYLRTSP 992
 QY 796 PTPASEATGAPTPPPAPPSPSAPPVVVPEKEEETAAAPP 836
 DB 993 HREGVRRRVPTTHPKPHRYQQPPVPRQIDDCPAKARP 1033

RESULT 98
 US-09-298-568-2
 ; Sequence 2, Application US/09298568
 ; Patent No. 6322792
 ; GENERAL INFORMATION:
 ; APPLICANT: Kieff, Elliott D.
 ; APPLICANT: Ballestar, Mary E.
 ; APPLICANT: Kaye, Kenneth M.
 ; TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
 ; FILE REFERENCE: 16412-1000IR
 ; CURRENT APPLICATION NUMBER: US/09/298,568
 ; CURRENT FILING DATE: 1999-04-21
 ; EARLIER APPLICATION NUMBER: US 60/109,422
 ; EARLIER FILING DATE: 1998-11-19
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 1162
 ; TYPE: PRT
 ; ORGANISM: Kaposi's sarcoma-associated herpesvirus
 US-09-298-568-2

Query Match 2.5%; Score 324; DB 4; Length 1162;
 Best Local Similarity 19.3%; Pred. No. 2.3e-10;
 Matches 135; Conservative 135; Mismatches 293; Indels 138; Gaps 18;

QY 146 EPVSP-----SPHTDPELEVPRLSKEELIONMDRVREITMVEQQLSKKKQ 197
 DB 461 EPLQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQ 520
 QY 198 QLEEEAAKPEPEKPVSPPIESKHSLSVLIYDNRKKAEEAHRILEGLGPQVELPLY 257
 DB 521 QQ--EPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQ 571
 QY 258 NQSDTRYHENIKINQAMRKLLIFKRNHARKQWKQFCORYDQLMALKKVERIE 317
 DB 572 REPQREP-----QQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQEQEPQ 612
 QY 318 NNPRRAKESKVREYKOPPEIRKQRELQERMQSRVQSGSLMSAARSEHVSIIID 377
 DB 613 DEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDE 669
 QY 378 GLSEQENLEKQMLQAVIPMLYDADQORIKFINMGLMADPMKYKDRQVMNWSQEK 437
 DB 700 ---QQDEQQDEQEQE-----QQDEQ-----QDEQQDEQQDEQQDEQQDE 700
 QY 438 ETPREKFMQHPKNGFLIASFLERKTVAECLVLYLTKNENYKSLVRRSRRRGKSGQQQ 497
 DB 701 EQQDEQQDEQEQE-----QQDEQ-----QDEQQDEQQDEQQDEQQDE 737
 QY 498 QQQQQQQQQQQQQMPRSSQEQEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKE 556

Best Local Similarity 19.3%; Pred. No. 2.3e-09;		Matches 353; Conservative 244; Mismatches 641; Indels 595; Gaps 83;	
QY	36	DVGLLEYQH-HSRDYASHLSPGS-----IIQPORRRRLSLLSEFOPGNERSOELHLRPEH 89	
Db	88	DVGQRESDVREKDRVDEMAANSTAVEDITKGOEETSEIIEIQIPASENNVEWQP-AE 146	
QY	90	SYLPELG-KSEMEFTI-----ESKRPRLELLPDLRLRPSLLATGQAPGSEDLTKD 138	
Db	147	SOANDVGFKKVFPVGFVKTKDKNEKSDTVQLL-----TVKKD 186	
QY	139	RSITGKLEPVSPSPPHDTDELE-LVPPRLSKZ-ELIONMDRVDRITWVEQQIS-----KL 193	
Db	187	E---GEGAEASVAGDHOEVSFETAVGASKESELKQSTK--QEGTLKQEOSSTEIPL 241	
QY	194	KKQOQLEEEAAKPPPEK-----PVSP-PPIESKHSRLVQIIVDEN-----RKKAEA 240	
Db	242	QAESDQAAEEAKDEGEKEKPTKSPSPSPVNSSETSSFKFPTHGAWGRKKTSP 301	
QY	241	AHRIEGLGPQVELPLYNQSPSTROYHENIKINQAMRKKLILYFKRHNHARKQWKQFCQ 300	
Db	302	KKSKEDDL-----ETAERKKEQEAESKVDSEKKEKTEPASEEQAEDTDQARLSA 351	
QY	301	RYDQLEALKKVERIENPRRAKESKVEYKQ--FPEIRKQRELQERMQSRGQ 358	
Db	352	DYKVELPLEDOVDLEASSEKCAPLATVDFDEKMEAHQEVVAEVHSTVTEEBEQG 411	
QY	359	SGLSMSAARSEHSEVSEIIDGLSQQENLEKQMRQLAVIPMLYDADQORIKFINMGLMAD 418	
Db	412	GG-----EAGGVVVEGTGES-----LPP-----EKIAE 435	
QY	419	PMKVYKDRQVMNMWSEOEKETFREKFM-----QHPKNFGLIA-- 455	
Db	436	PQEVPOE-----AEPABELMSREMCVSGDHTQLTDLSPBEKTLPKHPE--GIVSEV 486	
QY	456	---SFLERKTVAECVLYYITKQENYKSLVRYSRRGKSQQOQQOQQOQQOQQOQPM 512	
Db	487	EMLSQERIIVQGSPL-----KKLFSSGLKLS-----GKKQKRGGGDEBPGEYQHI 537	
QY	513	PRSQEKEDEKEKEAEKEEKEPEVENDKEDLLKEDTDSDGENDKEAVALSKGRKTA 572	
Db	538	HTSPSADQKGESSASSPEE-PE-----ETTCLEKGPLEAFQDGEABEGTSDGEK-- 589	
QY	573	NSQRRKGRITRMANEANEAEAITPOOASAEALSMELNESSRWTEEBEMETAKKGLLEHGR 632	
Db	590	-----KREG-----ITPWASFKKMWTPKKRVRRPS-----ESDK--ELEEKVKSATLSS-- 632	
QY	633	NWSAIARMVGSKTVSQCKNFYFNKQKQNLDEILQHKLKQEKERNARRKKKXAPAAASE 692	
Db	633	-----TDSTVSE-----MQDEVKTGVEQKPEEPKRRVDTSVSW 666	
QY	693	EAAPPPVVEDEMEASGVSGNEREMVEEAALHASGNEVPRGCSGPATVNNSSDTEIP 752	
Db	667	EALI--CVGSKKRARKASSDDE-----GGPRTLGGDSHRAE-----EASKKQKAGTDVAP 716	
QY	753	SPHTEAKDTGQNGKPPKPPATLGADGPPPGPP-----TPPRTSRAPIBPTPASEA 802	
Db	717	ASTQEQDQAQGSSSPEP-----AGSPSEGGVSTWESFKELVTPRKKSXKLE-EXAEDS 770	
QY	803	TGAPTPPPAPPS-----PSAP-----PPVV 822	
Db	771	SVQLSTEIPEPSREESWVSIKKIPGRKKRADGKQEQATVEDSGPVINEDDPNVPVAV 830	
QY	823	P-----KEEKEETAAAPP-----VEEGEEQK 844	
Db	831	PLSEYNAVEREKWEAQNTLPOLLGAVYVSELSKTLVHTVSVAVIDGTRAVTSVEERS 890	
QY	845	P-----PAAEELAVDTGKAPEPVKSECTEE---AEEGPA-----KXKDAEAAAEATAEGA 890	
Db	891	PSWISASVTEPLEHTAGEAMPVVE-EVTEKDIIAETPVLVTQLPEGKDAHDDDMVTSEVD 949	
QY	891	LKAEKKEGSGRATTAKSGAPQDSSTASATCSADEVDEAEGGDKNRLLSPRSLTPTGD 950	

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Job time : 223 secs

Db	950	FTSE-----AVTA-----TETSEALRTEEVTEASGAEBETDMVSAVSQLTDSPD 993	
QY	951	PRANASPOKD-----LDLKOLKORAAAIPIQVTKVHEPPREDAAAPTKPAPPAPPQNTL 1005	
Db	994	TTTEATPVQVEGVLDTHEEERQTQALLOAVADKVE-----ESQ 1034	
QY	1006	QPSDAPQOQSGSPRGKSRSPAPPADKEAPAAQAQLPGDPCCWTSGLPFPVPPREVIKA 1065	
Db	1035	VPATQTVORTGS--KALEKVEEVEDSEVLASEKEK-----1068	
QY	1066	SPHAPDPSAFSAPPCHPLPLGLHDHTARPVLPRPTTISNPPPLISSAKHPSVLERQIGAI 1125	
Db	1069	-----DVMRGPVQE-----AGAHE-----L 1084	
QY	1126	SOQMSVQLHVPYSEHAKAPVGPVTMGLP-LPMPDPKKLAPPSGVKOEOLSPRGQAGPPESL 1184	
Db	1085	AQG-----SETGOAT--PESLEVPETADVHDVATCQVIKLQQLME--QAVAPESS 1131	
QY	1185	GVPTAQEASVLRGTALGSVP-----GGSITKGIPSTRVPSDSAITY 1225	
Db	1132	ETLTDSETN-----GSTPLADSDTADGTQOQBETIDSQDSKATAAARQSVTEEAATA 1184	
QY	1226	R-----GSIHTGCTADVLVYKGTITRIIGEDSPSLDRGREDLSLPGHVIYEGKKGHVLSYE 1281	
Db	1185	QKEEPTSLPNNVPAQBEHGEPEGDRVLEPTQBELTAAAVPLAKTEVGOGE-----VDWL 1240	
QY	1282	GMMSVTQCKEDGSSSGPPHETAAPKRTYDM-----MEGRVGRAISSASI--EGLMGR 1333	
Db	1241	DGEKVE--EQEVFVHSGNSQKAADV-TYDSEVMGVAGQOEKESTEVQSLSEEGEMET 1297	
QY	1334	AIPPERH--SPHHLKEQHHRGSIOTIGIPRSYVEAQEDYLRRREAKLLKREGTPPPPPPSR 1391	
Db	1298	DVEKEKRETKPEQVSEEG-----EQETAAPAEHEGTYGKPVLT 1335	
QY	1392	DLTEAYKTQALGPKLKP-----AHEGLVATV--KEAG 1422	
Db	1336	DMPSSERKALGSLGSSPLPDQDKAGCIEVQVQSLDVTVTQTAEAVERKVIETVVISETG 1395	
QY	1423	RS-----IHEIPREE-----LRHTPE-LPLAPRPLKEGSIQTGP-----LKVDTG 1462	
Db	1396	ESPECVGAHLLPAEKSSATGGHWTLOHAEDTVLPGESQAESIPIIVTPAPESTLHDPDQ 1455	
QY	1463	ASTTGSKKGHVRSLLIGSPGRTPFPVPHPLDVMDARALERACYBESLSKSRP---GTASSSG 1519	
Db	1456	GEISASQRE-----RSEEDKP-DAGPDADGKESTAIEKVLKAEPEILELESKSN 1504	
QY	1520	GSTARCAPVIVPELGPQSPSLT--YEDHGAPFAGHLPRGSP-----VTMRETPR 1568	
Db	1505	KIVLNVIQTAVDQOFARTETAPETHAYDSQTVQACRLDSREPNCWTKMKDAKMKHPVQ 1564	
QY	1569	LQSG--SLSSSKA-SODRKLSTSTPREIAKSPPHS 1598	
Db	1565	PREDQLVTVLEAWAOPRK--CLPRLQKAPVS 1595	

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